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OM protein - protein search, using sw model
Run on: July 15, 2002, 12:46:44 ; Search time 29.22 Seconds
(without alignments)
95.032 Million cell updates/sec

Title: US-09-938-700-4
Perfect score: 136
Sequence: 1 CRYVHPHLPKDIVRSIKA PGKRAP 25
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 745754 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 253524
Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802,*

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22: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
SUMMARIES				
1	102	75.0	20	18 AA24102
				Canine immunoglobi
				Antibody 15A.2 bin
				Antibody 15A.2 can
				Optimized IgE-CH3
				Canine immunoglobi
				Antibody 15A.2 gre
				Antibody 15A.2 hum
				Optimized IgE-CH3
				Antibody 15A.2 swi
				Optimized IgE-CH3
				Modified human IgE
RESULT 1				
ID	AAW24102	standard:	peptide;	20 AA.
XX				
AC	AAW24102;			
XX				
DT	21-NOV-1997	(first entry)		
XX				
DE	canine immunogloblin E peptide 5.			
XX				
KW	Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.			
OS	Canis familiaris.			
XX				
PN	JP09169795-A.			
XX				
PD	30-JUN-1997.			
XX				
PF	22-DEC-1995;	95JP-0334381.		
XX				
PR	22-DEC-1995;	95JP-0334381.		
XX				
PA	(HITACHI CHEM CO LTD.			
XX				
DR	WPT: 1997-389423/36.			
DR	N-PSDB: AMX85651.			
XX				
PT	Canine immunoglobulin E peptide fragment and related DNA - useful			
PT	for the preparation of anti-canine immunoglobulin E antibody			
XX				
PS	Claim 2; Page 9; 12pp; Japanese.			
XX				
CC	AMW24098-106 are peptide fragments containing at least 5 continuous amino acids of the partial canine immunoglobulin E (IgE) protein shown			

CC in AAW24097. The peptides are used for the preparation of anti-canine IGE antibody. The anti-canine IGE antibody can be used for the diagnosis of canine allergies.

XX Sequence 20 AA;

RESULT 3
ID AAY50894 standard; peptide; 17 AA.
XX DE AAY50894;
AC XX DT 24-FEB-2000 (first entry)
XX DE Antibody 15A.2 canine IGE binding epitope 1.
XX KW Canine; allergy; antibody 15A.2; IGE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
XX OS Synthetic.
XX PN EP5711-A2.
XX XX PD 17-Nov-1999.
XX PP 09-APR-1999; 99EP-0107035.
XX PR 09-APR-1998; 98US-005831.
XX PR 30-MAR-1999; 99US-0281760.
XX PA (IDB-X) IDEXX LAB INC.
XX PI Lawton R, Mermier B, Francoeur G;
XX DR WPI; 2000-040833/04.
XX PT Binding proteins used for treatment or prophylaxis of canine allergy -
XX PS Disclosure; FIG 7; 30pp; English.
XX CC This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IGE, and which doesn't bind to IGE when the IGE is bound to mast cells. The peptide products of the invention have anti-allergen activity. The antibodies bind to defined epitopes on free or B-cell bound IGE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.
CC AAY50896-Y50900 represent peptide mimotopes used in the method of the invention.
XX SQ Sequence 17 AA;

Query Match 65.4%; Score 89; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRVTHPHLPDITRSI 16
Db 2 crvthphlpditorsi 17
OS Canis sp.

CC in AAW24097. The peptides are used for the preparation of anti-canine IGE antibody. The anti-canine IGE antibody can be used for the diagnosis of canine allergies.

XX Sequence 20 AA;

RESULT 3
ID AAY50894 standard; peptide; 17 AA.
XX DE AAY50894;
AC XX DT 24-FEB-2000 (first entry)
XX DE Antibody 15A.2 canine IGE binding epitope 1.
XX KW Canine; allergy; antibody 15A.2; IGE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
XX OS Synthetic.
XX PN EP5711-A2.
XX XX PD 17-Nov-1999.
XX PP 09-APR-1999; 99EP-0107035.
XX PR 09-APR-1998; 98US-005831.
XX PR 30-MAR-1999; 99US-0281760.
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XX DR WPI; 2000-040833/04.
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XX PS Disclosure; FIG 7; 30pp; English.
XX CC This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IGE, and which doesn't bind to IGE when the IGE is bound to mast cells. The peptide products of the invention have anti-allergen activity. The antibodies bind to defined epitopes on free or B-cell bound IGE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.
CC AAY50896-Y50900 represent peptide mimotopes used in the method of the invention.
XX SQ Sequence 17 AA;

Query Match 65.4%; Score 89; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRVTHPHLPDITRSI 16
Db 2 crvthphlpditorsi 17
OS Canis sp.

CC in AAW24097. The peptides are used for the preparation of anti-canine IGE antibody. The anti-canine IGE antibody can be used for the diagnosis of canine allergies.

XX Sequence 20 AA;

RESULT 3
ID AAY50894 standard; peptide; 17 AA.
XX DE AAY50894;
AC XX DT 24-FEB-2000 (first entry)
XX DE Antibody 15A.2 canine IGE binding epitope 1.
XX KW Canine; allergy; antibody 15A.2; IGE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
XX OS Synthetic.
XX PN EP5711-A2.
XX XX PD 17-Nov-1999.
XX PP 09-APR-1999; 99EP-0107035.
XX PR 09-APR-1998; 98US-005831.
XX PR 30-MAR-1999; 99US-0281760.
XX PA (IDB-X) IDEXX LAB INC.
XX PI Lawton R, Mermier B, Francoeur G;
XX DR WPI; 2000-040833/04.
XX PT Binding proteins used for treatment or prophylaxis of canine allergy -
XX PS Disclosure; FIG 7; 30pp; English.
XX CC This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IGE, and which doesn't bind to IGE when the IGE is bound to mast cells. The peptide products of the invention have anti-allergen activity. The antibodies bind to defined epitopes on free or B-cell bound IGE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.
CC AAY50896-Y50900 represent peptide mimotopes used in the method of the invention.
XX SQ Sequence 17 AA;

Query Match 65.4%; Score 89; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRVTHPHLPDITRSI 16
Db 2 crvthphlpditorsi 17
OS Canis sp.

CC in AAW24097. The peptides are used for the preparation of anti-canine IGE antibody. The anti-canine IGE antibody can be used for the diagnosis of canine allergies.

XX Sequence 20 AA;

RESULT 3
ID AAY50894 standard; peptide; 17 AA.
XX DE AAY50894;
AC XX DT 24-FEB-2000 (first entry)
XX DE Antibody 15A.2 canine IGE binding epitope 1.
XX KW Canine; allergy; antibody 15A.2; IGE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
XX OS Synthetic.
XX PN EP5711-A2.
XX XX PD 17-Nov-1999.
XX PP 09-APR-1999; 99EP-0107035.
XX PR 09-APR-1998; 98US-005831.
XX PR 30-MAR-1999; 99US-0281760.
XX PA (IDB-X) IDEXX LAB INC.
XX PI Lawton R, Mermier B, Francoeur G;
XX DR WPI; 2000-040833/04.
XX PT Binding proteins used for treatment or prophylaxis of canine allergy -
XX PS Disclosure; FIG 7; 30pp; English.
XX CC This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IGE, and which doesn't bind to IGE when the IGE is bound to mast cells. The peptide products of the invention have anti-allergen activity. The antibodies bind to defined epitopes on free or B-cell bound IGE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.
CC AAY50896-Y50900 represent peptide mimotopes used in the method of the invention.
XX SQ Sequence 17 AA;

Query Match 65.4%; Score 89; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRVTHPHLPDITRSI 16
Db 2 crvthphlpditorsi 17
OS Canis sp.

OS	Synthetic.	PA	(HITB) HITACHI CHEM CO LTD.
XX		XX	
PN	W0967293-A1.	DR	WPI; 1997-399423/36.
XX		N-PSDB;	AAT85652.
PD	29-DEC-1999.	XX	Canine immunoglobulin E peptide fragment and related DNA - useful
XX		PT	for the preparation of anti-canine immunoglobulin E antibody
PF	21-JUN-1999;	XX	
XX	99WO-US13959.	PS	
PR	20-JUN-1998;	XX	Claim 2; Page 9; 12pp; Japanese.
XX	98US-0100287.	XX	
PA	(UNBI-) UNITED BIOMEDICAL INC.	CC	AAW24098-106 are peptide fragments containing at least 5 continuous
XX		CC	amino acids of the partial canine immunoglobulin E (IgE) protein shown
PT	XX	CC	in AAW24097. The peptides are used for the preparation of anti-canine
Wang CY,	Walfield AM;	CC	IgE antibody. The anti-canine IgE antibody can be used for the diagnosis
XX		CC	of canine allergies.
DR		XX	
WPI:	2000-160578/14.	SQ	Sequence 20 AA;
PT	New antigenic peptide from the CH3 domain of immunoglobulin E, fusions		
XX	for immunization against allergy		
PS	Claim 1; Page 99; 155pp; English.		
XX			
CC	The present invention describes immunoglobulin E (IgE)-CH3 domain		
CC	antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic		
CC	and anti-asthmatic properties. (I) induces polyclonal antibodies		
CC	specific for a target effector site on the epsilon-heavy chain of IgE,		
CC	and so preventing triggering and activation of mast cells and basophils		
CC	and downregulation of IgE synthesis. Conjugates, or fusion peptides,		
CC	containing (I) are used for active immunisation against IgE-mediated		
CC	allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy		
CC	dermatitis. Nucleic acids that encode these compounds are useful for		
CC	recombinant production of corresponding peptides or in DNA vaccines.		
CC	Conjugates of (I) that include a promiscuous T helper cell epitope		
CC	(functional in genetically diverse subjects), in addition to a B cell		
CC	target epitope, have increased immunogenicity and may include cyclic		
CC	constraints (disulfide bridge) to stabilise conformational features and		
CC	maximize cross-reactivity to the natural target. They induce safe		
CC	(non-anaphylactogenic) antibodies. AAT79394 to AAY80084 represent amino		
CC	acid sequences used in the exemplification of the present invention.		
XX	Sequence 25 AA;		
SQ			
Query Match	58.1%	Score	79;
Best Local Similarity	100.0%	DB	18;
Matches	17;	Length	20;
Conservative	0;	Pred. No.	2.2e-05;
Mismatches	0;	Indels	0;
Indels	0;	Gaps	0;
Gaps	0;		
Oy	10 KDVRSIAKPGKRAP 25		
Db	1 kdivrsiakapgkrap 16		
RESULT	6		
ID	AAY5096		
XX	AAY50896 standard; peptide; 17 AA.		
AC	AAY50896;		
XX			
DT	24-FEB-2000 (first entry)		
XX			
DE	Antibody 15A.2 green monkey IgE binding epitope 1.		
XX			
KW	Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;		
KW	epitope; prophylaxis; treatment; mimotope.		
OS	Synthetic.		
XX			
PN	EP957111-A2.		
XX			
PD	17-NOV-1999.		
XX			
PF	09-APR-1999; 99EP-0107035.		
XX			
PR	09-APR-1998; 98US-0058331.		
PR	30-MAR-1999; 99US-0281760.		
XX			
PA	(IDEX-) IDEXX LAB INC.		
XX			
PI	Lawton R, Mermer B, Francoeur G;		
XX			
DR	WPI: 2000-040833/04.		
XX			
PT	Binding proteins used for treatment or prophylaxis of canine allergy -		
XX			
PS	Disclosure; Fig 7; 30pp; English.		
XX			
This invention describes a novel binding protein which specifically			
CC	binds to native canine free or B-cell bound IgE, and which doesn't bind		
CC	to IgE when the IgE is bound to mast cells. The peptide products of the		
PN	invention have anti-allergic activity. The antibodies bind to defined		
CC	epitopes on free or B-cell bound IgE molecules which have an important		
CC	role in allergic reaction. The specific binding proteins are used to		
CC	produce a pharmaceutical composition, preferably with a diluent, which		
CC	can be used for prophylaxis or treatment of canine allergy.		
CC	AAY50816-Y50900 represent peptide mimotopes used in the method of the		
XX			

SQ	Sequence	17 AA:
		AC XX
Query Match	52.9%; Score 72; DB 21; Length 17;	DT XX
Best Local Similarity	80.0%; Pred. No. 0.00022; Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	DE Optimised IgE-CH3 domain antigen peptide for rat IgE.
Qy	1 CRYVHPHLPKDVRs 15 : :	KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
Db	2 crvthphiphralvrs 16	KW Rattus sp. OS Synthetic. XX
RESULT	7	XX
ID	AY50895 standard; peptide; 17 AA.	PN W09967293-A1.
XX		XX
AC	AY50895;	PD 29-DEC-1999.
XX		XX
DT	24-FEB-2000 (first entry)	PF 21-JUN-1999; 99WO-US13959.
XX		XX
DE	Antibody 15A.2 human IgE binding epitope 1.	PR 20-JUN-1998; 98US-0100287.
XX		XX
KW	Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.	PA (UNBI-) UNITED BIOMEDICAL INC.
KW		XX
OS	Synthetic.	PI Wang CY, Walfield AM;
OS		XX
PN	EP95711-A2.	DR WPI: 2000-160578/14.
XX		XX
PD	17-NOV-1999.	PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy -
XX		XX
PF	09-APR-1999; 99EP-0107035.	PS Claim 1; Page 99; 155PP; English.
XX		XX
PR	09-APR-1998; 99US-0058331.	CC The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g., food allergies, asthma, anaphylaxis or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies: AAY7994 to AAY0084 represent amino acid sequences used in the exemplification of the present invention.
PR	30-MAR-1998; 99US-0281760.	CC XX
PA	(INDEX-) IDEXX LAB INC.	CC Sequence 25 AA;
XX		CC Sequence 25 AA;
PI	Lawton R, Mermer B, Francoeur G;	CC Sequence 25 AA;
XX		CC Sequence 25 AA;
DR	WPI: 2000-040833/04.	CC Sequence 25 AA;
XX		CC Sequence 25 AA;
PT	Binding proteins used for treatment or prophylaxis of canine allergy -	CC Sequence 25 AA;
XX		CC Sequence 25 AA;
PS	disclosure; Fig 7; 30PP; English.	CC Sequence 25 AA;
XX		CC Sequence 25 AA;
CC	This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.	CC Sequence 25 AA;
CC	CC invention.	CC Sequence 25 AA;
CC	CC AAY50876-Y50900 represent peptide mimotopes used in the method of the invention.	CC Sequence 25 AA;
XX		CC Sequence 25 AA;
SQ	Sequence 17 AA:	CC Sequence 25 AA;
Query Match	50.7%; Score 69; DB 21; Length 17;	Query Match Best Local Similarity 76.5%; Pred. No. 0.0014; Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Best Local Similarity	73.3%; Pred. No. 0.00065; Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	RESULT 9 AY50898 ID AAY50898 standard; peptide; 17 AA.
Qy	1 CRYVHPHLPKDVRs 15 : :	XX AY50898; XX AC AY50898; XX DT 24-FEB-2000 (first entry)
Db	2 crvthphiphralvrs 16	DE Antibody 15A.2 swine IgE binding epitope 1.
RESULT	8	XX
ID	AY80000 standard; Peptide; 25 AA.	XX

KW	Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;	PA	(UNBI-) UNITED BIOMEDICAL INC.	
XX	epitope; prophylaxis; treatment; mimotope.	XX		
OS		PT	Wang CY, Wallfield AM;	
XX	Synthetic..	XX		
PN	EP957111-A2.	DR	WPI; 2000-160578/14.	
XX		XX	New antigenic peptide from the CH3 domain of immunoglobulin E, fusions	
PD	17-NOV-1999.	PT	for immunization against allergy -	
XX		XX		
PF	09-APR-1999; 99EP-0107035.	PS	Claim 1; Page 21; 155pp; English.	
XX		XX		
PR	09-APR-1998; 98US-0058331.	CC	The present invention describes immunoglobulin E (IgE)-CH3 domain	
XX	30-MAR-1999; 99US-0281760.	CC	antigenic peptides (1). (1) have anti-allergic, anti-anaphylactic	
PA	(INDEX-) IDEXX LAB INC.	CC	and anti-asthmatic properties. (1) induces polyclonal antibodies	
XX		CC	specific for a target effector site on the epsilon-heavy chain of IgE,	
PI	Lawton R, Merner B, Francoeur G;	CC	and so preventing triggering and activation of mast cells and basophils	
XX		CC	and downregulation of IgE synthesis. Conjugates, or fusion peptides	
DR	DR; 2000-040833/04.	CC	containing (1) are used for active immunization against IgE-mediated	
XX		CC	allergies, e.g. food allergies, asthma, anaphylaxis, or flea allergy	
PT	Binding Proteins used for treatment or prophylaxis of canine allergy -	CC	dermatitis. Nucleic acids that encode these compounds are useful for	
XX		CC	recombinant production of corresponding peptides or in DNA vaccines	
PS	Disclosure; Fig 7; 30pp; English.	CC	conjugates of (1) that include a promiscuous T helper cell epitope	
XX		CC	(functional in genetically diverse subjects), in addition to a B cell	
CC	This invention describes a novel binding protein which specifically	CC	target epitope, have increased immunogenicity and may include cyclic	
CC	binds to native canine free or B-cell bound IgE, and which doesn't bind	CC	constraints (disulfide bridge) to stabilise conformational features and	
CC	to IgE when the IgE is bound to mast cells. The peptide products of the	CC	maximize cross-reactivity to the natural target. They induce safe	
CC	invention have anti-allergic activity. The antibodies bind to defined	CC	(non anaphylactogenic) antibodies. AAI79994 to AAI80084 represent amino	
CC	epitopes on free or B-cell bound IgE molecules which have an important	CC	acid sequences used in the exemplification of the present invention.	
CC	role in allergic reaction. The specific binding proteins are used to	XX		
CC	produce a pharmaceutical composition, preferably with a diluent, which	SQ	Sequence 25 AA;	
CC	can be used for prophylaxis or treatment of canine allergy.	Query Match	47.8%; Score 65; DB 21; Length 17;	
CC	AAV50816-Y50900 represent peptide mimotopes used in the method of the	Best Local Similarity	75.0%; Pred. No. 0.0027; 1; Mismatches 3; Indels 0; Gaps 0;	
XX	invention.	Matches		
XX	Sequence 17 AA;	Query Match	47.8%; Score 65; DB 21; Length 17;	
XX	Best Local Similarity	75.0%; Pred. No. 0.0027; 1; Mismatches 3; Indels 0; Gaps 0;	Best Local Similarity	64.7%; Pred. No. 0.006; 3; Mismatches 3; Indels 0; Gaps 0;
XX	Matches	Matches		
QY	1 CWRTHHLPKDVI16	QY	2 RVHHPHLKDVRSIAK 18	
	:		: :	
Db	2 cnytphdpdkpklrsi 17	Db	8 rvthphplrmrsttk 24	
RESULT 10	RESULT 11	Query Match	47.1%; Score 64; DB 21; Length 25;	
AYV79998	AYV91212	Best Local Similarity	64.7%; Pred. No. 0.006; 3; Mismatches 3; Indels 0; Gaps 0;	
ID AAV79998 standard; Peptide; 25 AA.	ID AAV91212 standard; peptide; 25 AA.	Matches		
XX	XX	Query Match	47.1%; Score 64; DB 21; Length 25;	
AC AYV79998;	AC AYV91212;	Best Local Similarity	64.7%; Pred. No. 0.006; 3; Mismatches 3; Indels 0; Gaps 0;	
XX	XX	Matches		
DT 15-MAY-2000 (first entry)	DT 22-MAY-2000 (first entry)	Query Match	47.1%; Score 64; DB 21; Length 25;	
XX	DE Modified human IgE CH3 domain, SEQ ID NO:92.	Best Local Similarity	64.7%; Pred. No. 0.006; 3; Mismatches 3; Indels 0; Gaps 0;	
DE Optimised IgE-CH3 domain antigen peptide for human IgE.	XX	Matches		
XX	Promiscuous T-cell epitope; measles virus F protein; MRF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; lutecising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMW; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; Plasmodium falciparum; circumsporozoite; antimalarial; CEPF; cholestryl ester transport protein; anti-arteriosclerotic.	Query Match	47.1%; Score 64; DB 21; Length 25;	
XX	OS Homo sapiens.	Best Local Similarity	64.7%; Pred. No. 0.006; 3; Mismatches 3; Indels 0; Gaps 0;	
OS Synthetic.	OS Synthetic.	Matches		
XX	XX	Query Match	47.1%; Score 64; DB 21; Length 25;	
Synthetic.	W09966957-A2.	Best Local Similarity	64.7%; Pred. No. 0.006; 3; Mismatches 3; Indels 0; Gaps 0;	
XX	PN W09967293-A1.	Matches		
XX	XX	Query Match	47.1%; Score 64; DB 21; Length 25;	
PD 29-DEC-1999.	PF 21-JUN-1999; 99WO-US13975.	Best Local Similarity	64.7%; Pred. No. 0.006; 3; Mismatches 3; Indels 0; Gaps 0;	
XX	XX	Matches		
PP 21-JUN-1999; 99WO-US13975.	PR 20-JUN-1998; 98US-0100412.	Query Match	47.1%; Score 64; DB 21; Length 25;	
XX	XX	Best Local Similarity	64.7%; Pred. No. 0.006; 3; Mismatches 3; Indels 0; Gaps 0;	
PR 20-JUN-1998; 98US-0100287.	PA (UNBI-) UNITED BIOMEDICAL INC.	Matches		
XX	XX	Query Match	47.1%; Score 64; DB 21; Length 25;	
XX	PT Wang CY;	Best Local Similarity	64.7%; Pred. No. 0.006; 3; Mismatches 3; Indels 0; Gaps 0;	
XX	Wang CY;	Matches		

XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
PS Example 6; Page 40; 12pp; English.

XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholestryl ester transport
CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
CC immuno-reactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HTV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone-
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
CC from the measles virus F (MVF) protein and sequences AY91122-91142,
CC AY91226 and AY91245-Y91246 represent syntetic Th epitopes based on the
CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AAY91144-Y9115 are synthetic epitopes derived from this HBV epitope.
CC AAY91156-Y91196, AAY91227 and AY91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AY91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AAY91200 is somatostatin, and AY91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AY91208 is a
CC human CD4 CDR2-like domain antigenic site, and AY91209-Y90211 are MVH Th
CC epitope/CD4 COR2 antigenic peptides which may be used to prevent HTV
CC infection of T cells. AY90212 is a modified version of a human IGE
CC (IgM immunoglobulin E) CH3 domain, and AY90213-Y90219 are Th epitope-IGE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AY91221-Y9122 comprise this peptide and a Th
CC epitope. AY91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AY91224-Y91225 comprise the CS antigen and an MVF Th
CC epitope and may be used in a malaria vaccine. AY91228-Y91231 represent
CC CERP-derived peptides and AY91222-Y91241 are immunogens comprising a
CC CERP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AY91247 and AY91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AY91248-Y91251 and
CC AY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.

XX
Sequence 25 AA:
SQ

Query Match 47.1%; Score 64; DB 21; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.006; ID XX
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 2 RYTHPHLPKDIVSIAK 18
Db |||||||: ::||| XX
8 rvthphlpkalmsttk 24 DT
XX DE Optimised IGE-CH3 domain antigen peptide for horse IGE.

RESULT 13
ID AAY80077
ID AAY80077 standard; Peptide; 25 AA.
XX AC AAY80077;
XX AY80077;
DT 15-MAY-2000 (first entry)
XX DE Optimised IGE-CH3 domain antigen peptide for horse IGE.

XX
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 OS Equus caballus.
 OS Synthetic.
 XX
 PN WO9967293-A1.
 XX
 PD 29-DEC-1999.
 PP 21-JUN-1999; 99WO-US13959.
 PR 20-JUN-1998; 98US-0100287.
 PA (UNIBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY, Walfield AM;
 XX
 DR WPI; 2000-160578/14.

PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -
 XX
 PS Claim 1; Page 146; 155pp; English.

The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE
 CC and so preventing triggering and activation of mast cells and basophils
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g., food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds may be useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe and
 CC effective (non-anaphylactogenic) antibodies. AAY9994 to AAY0084 represent amino
 SQ acid sequences used in the exemplification of the present invention.
 Sequence 25 AA;

Query Match
 Best Local Similarity 46.3%; Score 63; DB 21; Length 25;
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 VTHPHPLKDIVRSIAK 18
 ||::|| ||::|| |||||
 Db 9 vshpdplprevrsik 24

RESULT 15
 AAY42585; AAY42585 standard; peptide; 22 AA.
 AC AAY42585;
 XX DT 10-JAN-2000 (first entry)
 XX DE IgE peptide antagonist.
 XX KW Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;
 KW receptor-binding; binding determinant sequence; anti-IgE antibody;
 KW allergic disease.
 OS Homo sapiens.
 PN US5965709-A.
 XX PD 12-OCT-1999.
 PP 21-APR-1994; 94US-0233539.
 XX PR 14-AUG-1991; 91US-0744768.
 PR 07-JAN-1994; 94US-0178583.
 PA (GEETH) GENENTECH INC.
 XX PT Jardieu PM, Presta LG;
 XX DR WPI; 1999-579941/49.
 XX

PT Immunoglobulin E variants as peptide antagonists useful for raising and
PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
PT purification of FcepsilonRI receptor and in the treatment of allergic
PT diseases -
XX

PS Disclosure; Column 9; 37pp; English.

XX The invention provides immunoglobulin E (IgE) antagonists comprising one
CC or more of the FcepsilonRI receptor-binding determinant sites of human
CC IgE. The antagonists include IgE variants comprising an immunoglobulin
CC template and binding determinant sequences (bds) CDbs, ERbs and the
CC sequence shown in AAV42581. The CDbs (CD loop binding determinant
CC and sequence) are selected from the sequences shown in AAV42567-V42577 and
the ERbs (ER loop binding determinant sequence) are selected from
CC sequences shown in AAV42578-Y42580. The variants are useful in raising
CC and screening anti-IgE antibodies, in the isolation and purification of
CC FcepsilonRI receptor and in the treatment and prophylaxis of allergic
CC diseases.
XX

SQ Sequence 22 AA:

Query Match 44.1%; Score 60; DB 20; Length 22;
Best Local Similarity 69.2%; Pred. No. 0.021; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 3; Qy 1 CRYTHPHLUPKIV 13
Db 10 crvthphlupalm 22

Search completed: July 15, 2002, 12:50:18
Job time: 214 sec

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: July 15, 2002, 12:47:04 : Search time 12.87 Seconds
(without alignments) 47.447 Million cell updates/sec

Title: US-09-938-700-4
Perfect score: 136
Sequence: 1 CRYTHHLPKDIVRSIAKPGKRAP 25
Scoring table: BLOSUM62
Gappen 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425394 residues

Total number of hits satisfying chosen parameters: 134663

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
 1: /cgn2_6/prodata/2/1aa/5A.Comb.pep:*
 2: /cgn2_6/prodata/2/1aa/5B.Comb.pep:*
 3: /cgn2_6/prodata/2/1aa/6A.Comb.pep:*
 4: /cgn2_6/prodata/2/1aa/6B.Comb.pep:*
 5: /cgn2_6/prodata/2/1aa/PCRS_Comb.pep:*
 6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	47.1	25	3	US-09-100-414B-95
2	64	47.1	25	4	Sequence 95, Appl
3	60	44.1	22	2	Sequence 95, Appl
4	60	44.1	24	2	Sequence 95, Appl
5	60	44.1	24	2	Sequence 95, Appl
6	36	26.5	18	2	Sequence 95, Appl
7	36	26.5	22	2	Sequence 95, Appl
8	35	26.1	22	1	Sequence 95, Appl
9	35	26.1	22	2	Sequence 95, Appl
10	35	25.7	22	3	Sequence 95, Appl
11	35	25.7	22	4	Sequence 95, Appl
12	35	25.7	23	3	Sequence 95, Appl
13	35	25.7	23	4	Sequence 95, Appl
14	35	25.7	23	4	Sequence 95, Appl
15	35	25.7	23	4	Sequence 95, Appl
16	34	25.0	12	2	Sequence 95, Appl
17	34	25.0	21	2	Sequence 95, Appl
18	34	25.0	21	5	Sequence 95, Appl
19	34	25.0	20	1	Sequence 95, Appl
20	32	23.5	20	1	Sequence 95, Appl
21	32	23.5	20	2	Sequence 95, Appl
22	32	23.5	24	2	Sequence 95, Appl
23	32	23.5	24	4	Sequence 95, Appl
24	32	23.5	15	2	Sequence 95, Appl
25	31.5	23.2	15	2	Sequence 95, Appl
26	31.5	23.2	15	2	Sequence 95, Appl
27	31.5	23.2	15	2	Sequence 95, Appl

ALIGNMENTS

RESULT 1
US-09-100-414B-95
Sequence 95, Application US/09100414B
Patent No. 6025668

GENERAL INFORMATION:
 APPLICANT: Wang, Chang Yi
 TITLE OF INVENTION: NOVEL LHRH PEPTIDE
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan & Finnegan, L.L.P.
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10154-0054

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC Windows
 SOFTWARE: Word 97

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/100-414B
 FILING DATE: 20-JUNE-1998
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Maria H. Lin
 REGISTRATION NUMBER: 29-323
 REFERENCE DOCKET NUMBER: 1151-4157

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-758-0800
 TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-09-100-414B-95

Query Match 47.1%; Score 64; DB 3; Length 25;
 Best Local Similarity 64.7%; Pred. No. 0.0012; Indels 0; Gaps 0;
 Matches 11; Conservative 3; Mismatches 3;

Qy 2 RYTHHLPKDIVRSIAK 18
 Db ||||||| ::|||
 8 RYTHHLPLRMLRSTK 24

RESULT 2
US-09-303-323-95
; Sequence 95, Application US/09303323
; PATENT NO. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LRHH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Flanagan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-ARR-1999
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-95

Query Match Best Local Similarity 47.1%; Score 64; DB 4; Length 25;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 8 RYTHPHILPKDVK 18
Qy 2 RYTHPHILPKDVK 18
||||||| ::::|
Db 8 RYTHPHILPKDVK 24

RESULT 3
US-08-232-539D-19
; Sequence 19, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IGE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-APR-1994
CLASSIFICATION: 530

PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-3881

Query Match Best Local Similarity 44.1%; Score 60; DB 2; Length 22;
Matches 9; Conservative 69.2%; Pred. No. 0.0045; 1; Indels 0; Gaps 0;
Db 10 CRVTHPHLPRALM 22
Qy 1 CRVTHPHLPRALM 13
||||||| ::::|
Db 10 CRVTHPHLPRALM 22

RESULT 4
US-08-232-539D-20
; Sequence 20, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IGE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-APR-1994
CLASSIFICATION: 530

PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-3881

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-232-539D-20

Query Match 44.1%; Score 60; DB 2; Length 24;
Best Local Similarity 69.2%; Pred. No. 0.005; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPHPLPKDV 13
Db 12 CRVTHPHPLPKDV 24

RESULT 5
US-09-017-205-52
Sequence 52, Application US/09017205
; Patent No. 5965357

GENERAL INFORMATION:

APPLICANT: Marsden, Howard S
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN

TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5965357th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/017, 205

FILING DATE: 02-FEB-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mirchard, Leonard C
REGISTRATION NUMBER: 29, 009
TELEFAX: (703) 816-4000
REFERENCE/DOCKET NUMBER: 604-436

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4000

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

TOPOLOGY: Linear
MOLECULE TYPE: peptide from HSV-2 glycoprotein G
FRAGMENT TYPE: internal

US-09-017-205-52

Query Match 26.5%; Score 36; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 20; Mismatches 0; Indels 2; Gaps 0;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 THPHPKD 11
Db 7 THPHGPAD 14

RESULT 6
US-08-425-079-18

Sequence 18, Application US/084255079

Patent No. 594292

GENERAL INFORMATION:

APPLICANT: Tosato, Giovanna;
APPLICANT: Angiolillo, Anne L.; Sgadari, Cecilia
TITLE OF INVENTION: INTERFERON-INDUCIBLE
TITLE OF INVENTION: PROTEIN 10 IS A POTENT INHIBITOR OF
TITLE OF INVENTION: ANGIOGENESIS
NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5-INCH, 1.44 MB STORAGE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455, 079

FILING DATE: 31-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: KATHRYN M. BROWN

REGISTRATION NUMBER: 34, 556

REFERENCE/DOCKET NUMBER: 2026-4182

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 AMINO ACIDS

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PEPTIDE

US-08-455-079-18

Query Match 26.5%; Score 36; DB 2; Length 22;
Best Local Similarity 31.2%; Pred. No. 26; Mismatches 8; Indels 3; Gaps 0;

Matches 5; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 10 KDLVRSTAKAPGRKAP 25
Db 7 KNLUKAVSKEMSKRSP 22

RESULT 7

US-08-455-079-14
Sequence 14, Application US/08455079

Patent No. 594292

GENERAL INFORMATION:

APPLICANT: Tosato, Giovanna;

APPLICANT: Angiolillo, Anne L.; Sgadari, Cecilia

TITLE OF INVENTION: INTERFERON INDUCIBLE

TITLE OF INVENTION: PROTEIN 10 IS A POTENT INHIBITOR OF

TITLE OF INVENTION: ANGIOGENESIS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5-INCH, 1.44 MB STORAGE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455, 079

FILING DATE: 31-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: KATHRYN M. BROWN

REGISTRATION NUMBER: 34 556

REFERENCE/DOCKET NUMBER: 2026-4182

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 AMINO ACIDS

TYPE: AMINO ACID

TOPOLGY: LINEAR

MOLECULE TYPE: PEPTIDE

US-08-455-079-14

RESULT 8

US-07-988-925-12

; Sequence 12, Application US/07988925

; Patent No. 5585097

GENERAL INFORMATION:

APPLICANT: Bolt, Sarah L

APPLICANT: Clark, Michael R

APPLICANT: Gorman, Scott D

APPLICANT: Routledge, Edward G

APPLICANT: Waldmann, Herman

TITLE OF INVENTION: antibody preparation

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon and Vanderhye PC

STREET: 8th Floor, 1100 No. 5585097th Glebe Road

CITY: Arlington

STATE: Virginia

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/362,780

FILING DATE: 05-OCT-1990

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/862,543

FILING DATE: 23-JUNE-1992

APPLICATION NUMBER: GB 9021679.7

FILING DATE: 05-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB91/01726

ATTORNEY/AGENT INFORMATION:

NAME: Mitchell, Leonard C

REGISTRATION NUMBER: 29009

TELECOMMUNICATION INFORMATION:

TELEPHONE: 7038164000

TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLGY: linear

MOLECULE TYPE: peptide

US-08-362-780-12

RESULT 9

US-08-362-780-12

; Sequence 12, Application US/08362780

; Patent No. 5965509

GENERAL INFORMATION:

APPLICANT: Gorman, Scott D

APPLICANT: Routledge, Edward G

APPLICANT: Waldmann, Herman

TITLE OF INVENTION: Antibody Preparation

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon and Vanderhye PC

STREET: 8th Floor, 1100 No. 5968509th Glebe Road

CITY: Arlington

STATE: Virginia

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/362,780

FILING DATE: 05-OCT-1990

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/862,543

FILING DATE: 23-JUNE-1992

APPLICATION NUMBER: GB 9021679.7

FILING DATE: 05-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB91/01726

ATTORNEY/AGENT INFORMATION:

NAME: Mitchell, Leonard C

REGISTRATION NUMBER: 29009

TELECOMMUNICATION INFORMATION:

TELEPHONE: 7038164000

TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLGY: linear

MOLECULE TYPE: peptide

US-09-046-985-4

US-07-988-925-12

Query Match

Best Local Similarity 26.1%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPHLPKDVRSIKAQPK 22

Db 4 LTQPH-----SVSEICK 16

Query Match

Best Local Similarity 35.0%; Score 35.5; DB 1; Length 22;

Matches 7; Conservative 35.0%; Pred. No. 31; Mismatches 1

Sequence 4, Application US/09046985
 Patent No. 6121236
 GENERAL INFORMATION:
 APPLICANT: Ben-Sasson, Shmuel A.
 TITLE OF INVENTION: NOVEL MULTIVALENT LIGANDS WHICH MODULATE NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/09/474,743
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: 09/046,985
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: BROOK, DAVID E.
 REGISTRATION NUMBER: 22-592
 REFERENCE/DOCKET NUMBER: CMCC-614
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 861-6240
 TELEFAX: (781) 861-9540
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /label= "N-Acetyl Alanine"
 US-09-046-985-4

Query Match 25.7%; Score 35; DB 3; Length 22;
 Best Local Similarity 40.0%; Pred. No. 37; Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 Strands 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 HLPKDVRSIAKADG 21
 Db 8 HRPKDLYSTVRRADG 22

RESULT 12
 US-09-851-843A-208
 ; Sequence 208, Application US/08851843A
 ;
 Patient No. 6033809
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6093809el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/08/851,843A
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997

SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /label= "N-Acetyl Alanine"
 US-09-474-743-4

Query Match 25.7%; Score 35; DB 4; Length 22;
 Best Local Similarity 40.0%; Pred. No. 37; Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 Strands 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 HLPKDVRSIAKADG 21
 Db 8 HRPKDLYSTVRRADG 22

RESULT 12
 US-09-851-843A-208
 ; Sequence 208, Application US/08851843A
 ;
 Patient No. 6033809
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6093809el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/08/851,843A
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997

SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /label= "N-Acetyl Alanine"
 US-09-474-743-4

Query Match 25.7%; Score 35; DB 4; Length 22;
 Best Local Similarity 40.0%; Pred. No. 37; Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 Strands 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 HLPKDVRSIAKADG 21
 Db 8 HRPKDLYSTVRRADG 22

RESULT 12
 US-09-851-843A-208
 ; Sequence 208, Application US/08851843A
 ;
 Patient No. 6033809
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6093809el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/08/851,843A
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 013389-002930US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 208:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-851-843A-208

Query Match 25.7%; Score 35; DB 3; Length 23;
 Best Local Similarity 38.5%; Pred. No. 39;
 Matches 10; Conservative 1; Mismatches 3; Indels 12; Gaps 2;

Qy	4	THPH---LPKDIVRSIAKAPGRAP 25
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Db	6	TSPHPRNLQD-----PGPRCP 23

RESULT 13
 US-08-974-549A-327
 Sequence 327, Application US/08974549A
 Patent No. 6166178
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 172
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-Nov-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017

Query Match 25.7%; Score 35; DB 4; Length 23;
 Best Local Similarity 38.5%; Pred. No. 39;
 Matches 10; Conservative 1; Mismatches 3; Indels 12; Gaps 2;

Qy	4	THPH---LPKDIVRSIAKAPGRAP 25
		:
Db	6	TSPHPRNLQD-----PGPRCP 23

RESULT 14
 US-08-854-050-208
 Sequence 208, Application US/08854050
 Patent No. 6261836
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6261836el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854, 050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851, 843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846, 017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844, 419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724, 643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
FORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
-854-050-208

T 15
T 430-323-208
REFERENCE: 208, Application US/09430323
ENT No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lindner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/774,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429

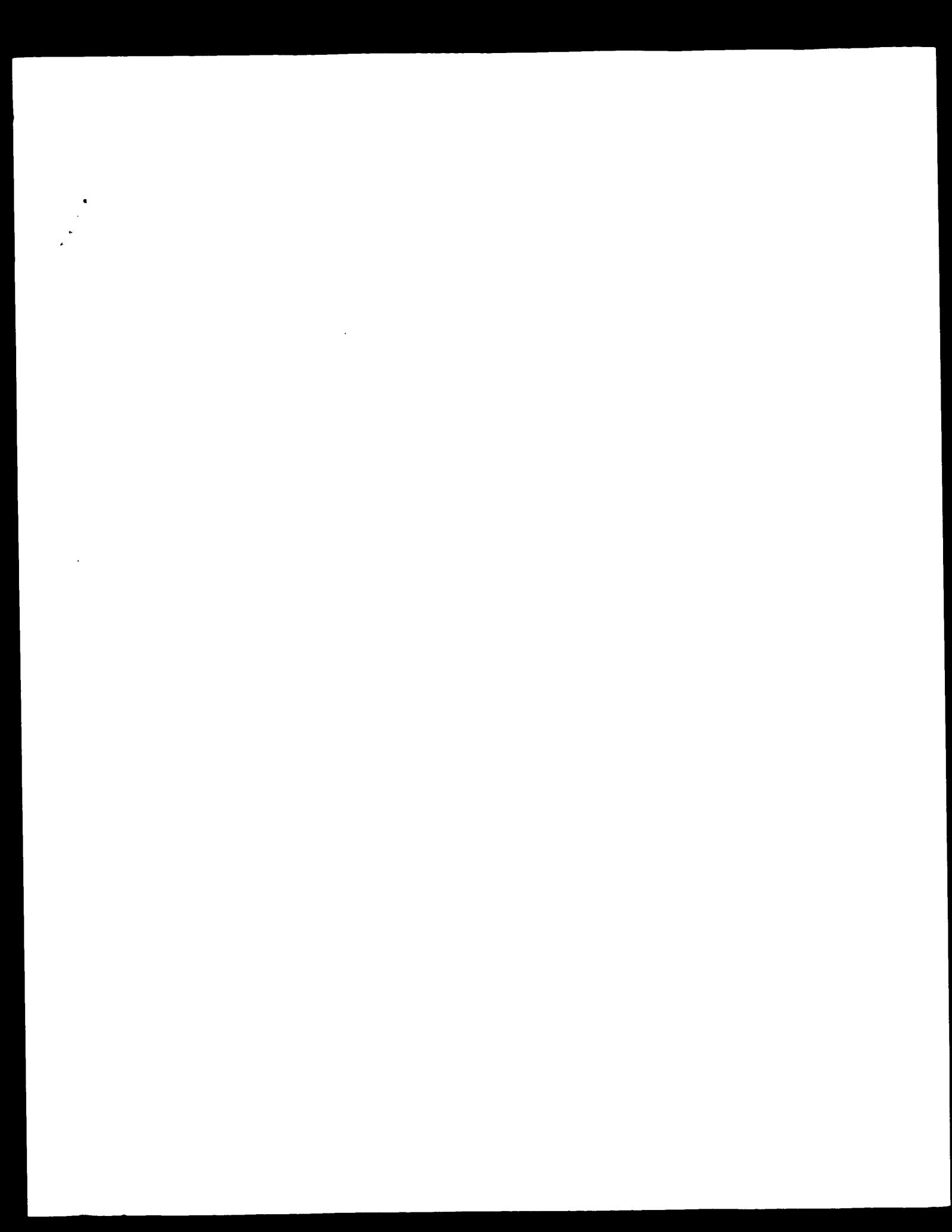
REFERENCE/DOCKET NUMBER: 015309-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 208:

SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 208:

US-09-430-323-208

Query Match Best Local Similarity Score 35; DB 4; Length 23;
Matches 10; Conservative 1; Mismatches 3; Indels 12; Gaps 2.



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Run on:	July 15, 2002, 12:48:59 ; Search time 14-14 seconds (without alignments) {169.889 Million cell} updates/sec			
Title:	US-09-938-700-4			
Perfect score:	136			
Sequence:	1 CRYTHPHPLPKDIVRSIAKAPGKRAP 25			
Scoring table:	BLOSUM62			
	Gapop 10.0 , Gapext 0.5			
Searched:	283138 seqs, 96089334 residues			
Total number of hits satisfying chosen parameters:	4981			
Minimum DB seq length:	0			
Maximum DB seq length:	25			
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries			
Database :	PIR_71;*			
	1: pir1;*			
	2: pir2;*			
	3: pir3;*			
	4: pir4;*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description
1	29	21.3	25	histone H2B, 1, sperm - sea urchin (<i>Echinus esculentus</i>) (fragment)
2	28	20.6	11	ribosomal protein
3	27	19.9	16	Ig heavy chain DJ
4	27	19.9	2	acid ribonuclease
5	27	19.9	25	gene J protein - p granulocyte inhibi
6	26.5	19.5	20	lysophosphatidylserine kinase
7	26.5	19.5	22	polyalacturonase
8	26	19.1	13	glutathione transf
9	26	19.1	15	ribosomal protein
10	26	19.1	20	hypothetical TELM
11	26	19.1	22	Ig kappa chain VI
12	26	19.1	22	Ig kappa chain V-I
13	26	19.1	24	ribosomal protein
14	26	19.1	24	bradykinin-potenti
15	25	18.4	10	superoxide dismuta
16	25	18.4	15	agrin - electric r
17	25	18.4	17	bombolitin IV - An
18	25	18.4	20	flagellar motor sw
19	25	18.4	20	ribosomal protein
20	25	18.4	21	glutamate--ammonia
21	25	18.4	21	kinetoplast DNA as
22	25	18.4	22	hypothetical prote
23	25	18.4	24	somatotropin - Atl
24	25	18.4	25	bradykinin-potenti
25	24	17.6	10	outer layer protei
26	24	17.6	20	retinoid-X-recepto
27	24	17.6	21	ribosomal protein
28	24	17.6	22	hypothetical prote
29	24	17.6	22	
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		Db	4	KSPTKRSP 11
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Best Local Similarity 62.5%; Pred. No. 1.3e+03; 1; Indels 0; Gaps 0;				
Matches 5; Conservative 2; Mismatches 1;				
C;Species: <i>Echinus esculentus</i> sequence_revision 30-Sep-1991 #text_change 23-Feb-1997				
C;Date: 30-Sep-1991 #sequence_change 23-Feb-1997				
C;Accession: S07770				
R;Hill, C.S.; Thomas, J.O.				
Eur. J. Biochem. 187, 145-153, 1990				
A;Title: Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal				
A;Reference number: S07765; MUID:9016812				
A;Accession: S07770				
A;Molecule type: protein				
A;Residues: 1-25 <HTML>				
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C;Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus				
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Best Local Similarity 40.0%; Pred. No. 7.7e+02; 0; Gaps 0;				
Matches 4; Conservative 3; Mismatches 3; Indels 0;				
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RESULT	3			

PH1351
Ig heavy chain DJ region (clone C100-109B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
R;Massemann, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PH1302; MUID:93094761
A;Accession: PH1351
A;Molecule type: DNA
A;Residues: 1-16 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 19.9%; Score 27; DB 2; Length 16;
Matches 5; Conservative 0; Pred. No. 1.6e+03; Mismatches 5; Indels 0; Gaps 0;

Qy 16 IAKAPKRKAP 25
Db 7 IGSTPPGAREP 16

RESULT 4

A41439
acid ribonuclease (EC 3.1. -.-) - bovine (fragment)
C;Species: Bos primigenius tauris (cattle)
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Mar-1996
C;Accession: A41439
R;Ohta, K.; Sanda, A.; Takikawa, Y.; Irie, M.
J. Biochem. 103, 267-273, 1988
A;Title: Purification of acid ribonucleases from bovine spleen.
A;Reference number: A41439; MUID:88227899
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <OIG>
C;Keywords: hydrolase

Query Match
Best Local Similarity 19.9%; Score 27; DB 2; Length 20;
Matches 4; Conservative 0; Pred. No. 2.e+03; Mismatches 2; Indels 5; Gaps 1;
Indels 0; Gaps 0;

Qy 5 HPHLPRKDI 12
Db 9 HLFPPKDL 16

RESULT 5

ZJBPG4
gene J protein - phage G4
C;Species: phage G4
C;Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 28-Jul-2000
C;Accession: A04259
R;Godson, G. N.; Barrell, B. G.; Staden, R.; Fiddes, J. C.
Nature 276, 236-247, 1978
A;Title: Nucleotide sequence of bacteriophage G4 DNA.
A;Reference number: A93200; MUID:79053264
A;Accession: A04259
A;Molecule type: DNA
A;Residues: 1-25 <GOD>
A;Cross-references: GB:J02454; GB:MI0724; GB:MI1104; GB:V00657; MUID:915831; PIDN:CAA2401
C;Comment: Gene J protein is one of the structural components of the bacteriophage coat.
C;Superfamily: phage phi-X174 gene J protein
C;Keywords: DNA binding

Query Match
Best Local Similarity 19.9%; Score 27; DB 1; Length 25;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 19.9% 27 1 25 7 2 7 0 0

Qy 8 LPKDIVRSIAKAPGKR 23
Db 1 MKSIRRSGGSKSGAR 16

RESULT 6

A36016
granulocyte inhibitory protein - human
C;Species: Homo sapiens (man)
C;Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 30-May-1997
C;Accession: A36016
R;Hoerl, W.H.; Haag-Weber, M.; Georgopoulos, A.; Block, L.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 633-6357, 1990
A;Title: Physicochemical characterization of a polypeptide present in uremic serum th

A;Reference number: A36016; MUID:90349614
A;Accession: A36016
A;Molecule type: protein
A;Residues: 1-20 <HOE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match

Best Local Similarity 19.5%; Score 26.5; DB 2; Length 20;
Matches 7; Conservative 5; Mismatches 2; Indels 5; Gaps 1;

Qy 11 DIVR----SIKAKGKA 24
Db 1 DIVMTQSPTGLSVSGERA 19

RESULT 7

P0143
polygalacturonase (EC 3.2.1.15) P26 - evening primrose (fragment)
C;Species: Oenothera organensis (evening primrose)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 06-Dec-1996
C;Accession: P0143
R;Brown, S.M.; Crouch, M.L.
Plant Cell 2, 263-274, 1990

A;Title: Characterization of a gene family abundantly expressed in Oenothera organensis
A;Reference number: JQ0992; MUID:93005658
A;Accession: P0143
A;Molecule type: mRNA
A;Residues: 1-22

A;Experimental source: pollen
C;Comment: This protein is specifically translated in the pollens. cell walls of the pollen growing tube.
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match
Best Local Similarity 19.5%; Score 26.5; DB 2; Length 22;
Matches 8; Conservative 3; Mismatches 9; Indels 1; Gaps 1;
Indels 0; Gaps 0;

Qy 1 CRVTHHLPLPDIVRSIAKAPG 21
Db 1 CTITNAQL-FDITYKGAKGD 20

RESULT 8

S3251
glutathione transferase (EC 2.5.1.18) mu (isoform pI 6.4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 05-Jan-1995
C;Accession: S3251; S3250
R;Singhal, S.S.; Sexena, M.; Ahmad, H.; Awasthi, Y.C.
Biochim. Biophys. Acta 1116, 137-146, 1992
A;Title: Glutathione S-transferase of mouse liver: sex-related differences in the ex
A;Reference number: S32548; MUID:92256466
A;Accession: S3251
A;Molecule type: protein
A;Residues: 1-13 <SNL>

A;Experimental source: female
A;Accession: S32550
A;Molecule type: protein
A;Residues: 1-13 <SN2>
A;Experimental source: male
C;Keywords: transferase

Query Match Best Local Similarity 19.1%; Score 26; DB 2; Length 13;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RYTHP 6
Db 9 RLTHP 13

RESULT 9

I38336 hypothetical TBL/MNL mutant fusion protein type I - human (fragment)
C;Species: Homo sapiens (man)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000

C;Accession: I38336 R.Buijs, A.; Sherr, S.; van Baal, S.; van der Plas, D.; Van Kessel, A.G.

Oncoogene 10, 1511-1519, 1995

A;Title: Translocation (12;22) (P13;q11) in myeloproliferative disorders results in fusi

A;Reference number: I38031; MUID:95249265

A;Status: translated from GB/EMBL/DBDJ

A;Residues: 1-15 <BUI2>

A;Cross-references: EMBL:X85026; NIN:991473; PID:991474

C;Comment: This sequence is the chimeric product of a translocation mutation.

A;Gene: ERV6/MNL; TEL/ANL

A;Map position: 22q11.1/2p13

C;Keywords: fusion protein

Query Match Best Local Similarity 19.1%; Score 26; DB 4; Length 15;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 HLPKDI 12
Db 6 HLPHD 11

RESULT 10

JP0055 ribosomal protein L30 - Bacillus polymyxa (fragment)

C;Species: Bacillus polymyxa
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 02-Sep-2000

R;Ochi, K.
submitted to JRPD, February 1994

A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr

A;Reference number: JP0042
A;Accession: JP0055

A;Molecule type: protein
A;Residues: 1-20 <OCH>

C;Superfamily: Escherichia coli ribosomal protein L30
C;Keywords: protein biosynthesis; ribosome

Query Match Best Local Similarity 19.1%; Score 26; DB 2; Length 20;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 12 IVRSIAKAPG 21
Db 7 LVRSILGRPG 16

RESULT 11

H30608 Ig kappa chain V-III region (SHe) - human (fragment)

C;Accession: H30608 Ig kappa chain V-III region (SHe) - human (fragment)

C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997

R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S

J. Immunol. 142, 3158-3163, 1989

A;Title: Structural and idiotypic characterization of the L chains of human IgM auto

A;Reference number: A30601; MUID:8921279

A;Accession: H30608 A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <GON>

C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 19.1%; Score 26; DB 2; Length 22;

Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 15 SIAKAPKRA 24
Db 10 TLSVSPGERA 19

RESULT 12

D30609 Ig kappa chain V-III regions (Jon and Mitt) - human (fragment)

C;Accession: D30609 Ig kappa chain V-III regions (Jon and Mitt) - human (fragment)

C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997

R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S

J. Immunol. 142, 3158-3163, 1989

A;Title: Structural and idiotypic characterization of the L chains of human IgM auto

A;Reference number: A30601; MUID:89215279

A;Accession: D30609 A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <GON>

C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 19.1%; Score 26; DB 2; Length 22;

Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 15 SIAKAPKRA 24
Db 10 TLSVSPGERA 19

RESULT 13

B30609 Ig kappa chain V-III region (She) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997

C;Accession: B30609 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S

J. Immunol. 142, 3158-3163, 1989

A;Title: Structural and idiotypic characterization of the L chains of human IgM auto

A;Reference number: A30601; MUID:89215279

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-24 <GON>

C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 24;
 Best Local Similarity 40.0%; Pred. No. 3.3e+03; Mismatches
 Matches 4; Conservative 5; Indels 0; Gaps 0;

Qy 15 SIAKAPGKRA 24
 :: :||:||
 Db 10 TLSVSPGERA 19

RESULT 14

JP0052 ribosomal protein L30 - *Bacillus macquariensis* (fragment)

C;Species: *Bacillus macquariensis*

C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 02-Sep-2000

C;Accession: JP0052

R;Oehl, K.

submitted to JIPD, February 1994

A;Description: Phylogenetic diversity in the genus *Bacillus* and comparative ribosomal pr

A;Reference number: JP0042

A;Accession: JP0052

A;Molecule type: protein

A;Residues: 1-24 <OCH>

C;Superfamily: *Escherichia coli* ribosomal protein L30

C;Keywords: protein biosynthesis; ribosome

Query Match 19.1%; Score 26; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 3.3e+03; Mismatches
 Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 12 TYRSTAKAPG 21
 :||:|||:
 Db 8 LVRSLIGRPG 17

RESULT 15

H37196 bradykinin-potentiating peptide 8 - island Jararaca

C;Species: Bothrops insularis (island Jararaca)

C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994

C;Accession: H37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides from

A;Reference number: A37196; MUID:90351557

A;Accession: H37196

A;Status: Preliminary

A;Molecule type: protein

A;Residues: 1-10 <CTNS>

C;Keywords: pyroglutamic acid (Gln) #status experimental
 F;1/Modified site: Pyrrolidine carboxylic acid (Gln) #status experimental

Query Match 18.4%; Score 25; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.9e+03; Mismatches
 Matches 3; Conservative 2; Indels 0; Gaps 0;

Qy 5 HPHLP 9
 ||:||:
 Db 5 HPNIP 9

Search completed: July 15, 2002, 12:50:59
 Job time: 120 sec

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Om protein - protein search, using sw model

Run on: July 15, 2002, 12:50:44 ; Search time 10-22 seconds
(without alignments)
{4.715 Million cell updates/sec}

Title: US-09-938-700-4
perfect score: 136

Sequence: 1 CRYTHPHHLPRDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 10324 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 1503

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	31	22.8	18	1	CTIC_LITCI	P81844	litoria cit
2	29	21.3	18	1	CTIC_LITCI	P81838	litoria cit
3	29	21.3	25	1	H2BL_ECHES	P1381	echinus esc
4	27	19.9	12	1	PPK4_PERAM	P82019	periplaneta
5	27	19.9	24	1	DMS5_PVBIT	P81490	phyllomedusa
6	27	19.9	25	1	VGJ_BPG4	P03052	bacteriophaga
7	26.5	19.5	19	1	TRP3_LDEMA	P81135	leucophaga
8	26	19.1	13	1	UP71_LITEW	P82050	litoria ewi
9	25	19.1	15	1	UC05_MAIZE	P80612	zea mays (m)
10	26	19.1	16	1	CT12_LITCI	P81840	litoria cit
11	19.1	18	1	1	CTID_LITCI	P81845	litoria cit
12	25	18.4	10	1	BPP8_BOTTIN	P30426	bothrops in
13	25	18.4	13	1	AU11_LITRA	P82386	litoria ran
14	25	18.4	15	1	MCA2_RHOOP	P56870	rhodococcus
15	25	18.4	16	1	CT13_LITCI	P81946	litoria cit
16	25	18.4	17	1	BOLM_MEGRE	P07195	megabombus
17	25	18.4	19	1	TRPB_KLERA	P14552	klebsiella
18	25	18.4	20	1	RUCI_HAIMA	P12740	haloarcula
19	18.4	25	1	CR23_LITCE	P56235	litoria cae	
20	25	18.4	25	1	CR24_LITCE	P56236	litoria cae
21	25	18.4	21	1	BPP2_BOTTIN	P30422	bothrops in
22	24	17.6	10	1	MA0X_CHICK	P02000	gallus gallus
23	24	17.6	16	1	AU22_LITPAU	P82389	litoria aur
24	24	17.6	16	1	AU23_LITAU	P82390	litoria aur
25	24	17.6	16	1	CT11_LITCI	P81835	litoria cit
26	24	17.6	16	1	H5_COTJA	P18638	coturnix co
27	24	17.6	17	1	AU31_LITRA	P82394	litoria ran
28	24	17.6	17	1	AU32_LITRA	P82395	litoria ran
29	17	17.6	17	1	AU33_LITRA	P82396	litoria ran
30	24	17.6	18	1	CT1B_LITCI	P81839	litoria cit
31	24	17.6	20	1	WMO2_CHICK	OPPS39	gallus gallus
32	24	17.6	23	1	NIFD_ANASL	P33177	anaabaena sp

ALIGNMENTS

RESULT 1	CTIC_LITCI	STANDARD;	PRT;	18 AA.
ID	CTIC_LITCI			
AC	P81844			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Citropin 1.2.4.			
DR	citropin			
EC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Battacharia; Anura; Neobatrachia; Bufonoidea; Hylidae;			
OC	litoria;			
OX	NCBI_TaxID=94770;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Skin;			
RX	MDLINE=9433977; PubMed=10504394;			
RA	Wagener K.L., Wabnitz P.A., Carver J.A., Chia B.C.S., Wallace J.C., Tyler M.J.;			
RA	"Host defence peptides from the skin glands of the Australian blue tree-frog Litoria citropa. Solution structure of the antibacterial peptide citropin 1.1.";			
RA	Erir. J. Biochem. 265:677-637(1999).			
CC	-1_TISSUE_SPECIFICITY: DORSAL AND SUBMENTAL SKIN GLANDS.			
SQ	SEQUENCE 1B_AA; 1814 MW; 500BF778D515ABD7 CRC64;			

Query Match 22.8%; Score 31; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 1.7e+02; 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0; Qy 11 DIVRSIAKAPGKRAP 25

Db 4 DIKKVAVSVGLASP 18

RESULT 2	CTIA_LITCI	STANDARD;	PRT;	18 AA.
ID	CTIA_LITCI			
AC	P81838;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Cirropon 1.1.3.			
DR	Cirropon 1.1.3.			
EC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batracchia; Anura; Neobatrachia; Bufonoidea; Hylidae;			
OC	Bukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Litoria.			
OC	litoria.			
OX	NCBI_TaxID=94770;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Skin;			
RX	MDLINE=9433977; PubMed=10504394;			
RA	Weigener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S., Wallace J.C., Tyler M.J.;			
RA	"Host defence peptides from the skin glands of the Australian blue tree-frog Litoria citropa. Solution structure of the antibacterial peptide citropin 1.1.";			
RA	Erir. J. Biochem. 265:677-637(1999).			

RT mountains tree-frog *Litoria citropa*; Solution structure of the
 RT antibacterial peptide citrogin 1.1.;
 RL Eur. J. Biochem. 265:627-637(1999).
 CC -!- TISSUE SPECIFICITY: DORSAL AND SUBMENIAL SKIN GLANDS.
 SEQUENCE 18 AA; 1814 MW; 500BF778051F96D7 CRC64;

Query Match 21.3%; Score 29; DB 1; Length 18;
 Best Local Similarity 26.7%; Pred. No. 3.3e+02;
 Matches 4; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 SQ 11 DIVRSIKAQGRRAP 25
 |::: ;| :| :| :| :|
 4 DVIRKKVASVIGLASP 18

RESULT 3

HBL_ECHES STANDARD; PRT; 25 AA.

ID H2B1_ECHES
 AC P13281;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Histone H2B.1, sperm (fragment).
 OS Echininus esculentus (Sea urchin).
 OC Echinoidea; Euechinoidea; Echinacea; Echinida; Echinidae; Echinus.
 OX NCBI_TaxID=7648;
 RN [1]
 RP SEQUENCE:
 RX MEDLINE=90126812; PubMed=2298202;
 RA Hill C.S., Thomas J.O.;
 RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal tail of H2B interacts with linker DNA.";
 RL Eur. J. Biochem. 107:145-153(1990).
 CC -!- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 146 BP OF DNA.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.
 DR PIR: S07770; S07770
 DR InterPro: IPR000558; HISTONE_H2B.
 DR PROSITE: PS00357; HISTONE_H2B; PARTIAL.
 KW Nuclear Protein; Chromosomal protein; Nucleosome core; DNA-binding;
 KW Multigene family.
 FT NON_TER 25 AA;
 SQ SEQUENCE 25 AA; 2693 MW; 98420D3D73A3A9EC CRC64;

Query Match 21.3%; Score 29; DB 1; Length 25;
 Best Local Similarity 62.5%; Pred. No. 4.6e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 SQ 18 KAPGKRAP 25
 |:| |||:
 Db 4 KSPTKNSP 11

RESULT 4

PPKA_PERAM STANDARD; PRT; 12 AA.

ID PPK4_PERAM
 AC PRB619;
 DT 15-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pyrokinin-4 (Peptide-PK-4) (IXPL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RESULT 5

DMS6_PHIBI STANDARD; PRT; 24 AA.

ID DMS6_PHIBI
 AC P81190;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Dermaseptin BVI (Dermaseptin BG).
 OS Phyllomedusa bicolor (Two-colored leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyliidae; Phyllomedusa.
 OX NCBI_TaxID=8393;
 RN [1]
 RP SEQUENCE:
 RX MEDLINE=98278974; PubMed=9614066;
 RA Charnier S., Amiche M., Mester J., Vouille V., Le Caer J.-P., Niclou P., Defoix A.;
 RT "Structure, synthesis, and molecular cloning of dermaseptins B, a family of skin peptide antibiotics.";
 RL J. Biol. Chem. 273:14650-14657(1998).
 CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE DERMASEPTIN FAMILY.
 FT MOD-RES 24 24 AMIDATION (POVETAIL).
 SQ SEQUENCE 24 AA; 2665 MW; E5987D750E08F4F CRC64;

Query Match 19.9%; Score 27; DB 1; Length 24;
 Best Local Similarity 50.0%; Pred. No. 8.5e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 SQ 10 KOJVRSAKA 19
 ||||:
 Db 4 KDLKNAGKA 13

RESULT 6

VGJ_BPG4 STANDARD; PRT; 25 AA.
 ID VGJ_BPG4
 AC P03652;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Small core protein (J protein).
 J. Bacteriophage G4.
 OS Bacteriophage G4.
 OC Viruses; ssDNA viruses; Microviridae; Microvirus.
 OX NCBI_TaxID=10843;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9053264; PUBMED=714153;
 RA Godson G.N., Barrell B.G., Staden R., Fiddes J.C.;
 RT "Nucleotide sequence of bacteriophage G4 DNA.";
 RL Nature 276:236-247(1978).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=6217890; PUBMED=8642594;
 RA McKenna R., Bowman B.R., Tagg L.L., Rossmann M.G., Fane B.A.;
 RT "Atomic structure of the degraded proicosmid particle of the
 bacteriophage G4: induced structural changes in the presence of
 calcium ions and functional implications.";
 RT J. MOL. BIOL. 250:736-750(1996).
 CC -I- FUNCTION: THE J PROTEIN IS ASSOCIATED WITH THE DNA AND IS SITUATED
 IN AN INFERIOR CLEFT OF THE F PROTEIN.
 CC -I- SUBUNIT: THE VIRION IS COMPOSED OF 60 COPIES EACH OF THE F, G, AND
 J PROTEINS, AND 12 COPIES OF THE H PROTEIN.
 CC -----
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 CC -----
 DR EMBL; J02454; AAA32322.1; .
 DR EMBL; V00057; CA24018.1; .
 DR PTR; A04259; ZJBPG4
 DR PDB; 1GF5; 03-APR-96
 KW Coat protein; DNA-binding; 3D-structure;
 SEQUENCE ; 25 AA; 2815 MW; 87B/ABDFFED6D033 CRC64;

RESULT 8 UP71_LITEW STANDARD; PRT; 13 AA.
 ID UP71_LITEW
 AC PR2050;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Uperin 7.1 (contains: UPERIN 7.1.1).
 OS Litoria ewingii (Brown tree frog) (Ewing's tree frog),
 Eukarriota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104896;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinbocker S.T., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "An unusual combination of peptides from the skin glands of Ewing's
 tree frog, Litoria ewingii. Sequence determination and antimicrobial
 activity.";
 RL Aust. J. Chem. 50:889-894(1997).
 CC -I- FUNCTION: UPERIN 7.1 SHOWS ANTIMICROBIAL ACTIVITY AGAINST L. LACTIS
 CC AND S. UBERIS. UPERIN 7.1.1 IS INACTIVE.
 CC -I- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -I- MASS SPECTROMETRY: MW=1427; METHOD=FAB; RANGE=1-13.
 KW Amphibian skin; Antibiotic; Amidation.
 FT PEPTIDE 1 13 UPERIN 7.1.
 FT PEPTIDE 3 13 UPERIN 7.1.1.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1429 MW; DEL7C7204CCAE322 CRC64;

RESULT 7 TRP3_LEUMA STANDARD; PRT; 19 AA.
 ID TRP3_LEUMA
 AC P81735;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Tachykinin-related peptide 3 (LeuTRP 3).
 OS Leucophphaea mederae (Maderia cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophphaea.
 RN [1]
 RP SEQUENCE;
 RC TISSUE=Midgut;
 RX MEDLINE=97053012; PUBMED=8897641;
 RA Muren J.E., Naessel D.R.;

RESULT 9 UC06_MAIZE STANDARD; PRT; 15 AA.
 ID UC06_MAIZE
 AC P80612;
 DT 01-OCT-1995 (Rel. 34, Created)
 DT 01-OCT-1995 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (spot 1131)
 DE (Fragment).

CC -!- AMPHIPATHIC STRUCTURE. SHOWS ANTICANCER ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 KW Amidation; Antibiotic.
 FT M02_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1481 MW; 1ERCB9DFBC83330 CRC64;

RESULT 13
 ID AU11_LITRA STANDARD; PRT; 13 AA.
 AC P82386;
 DT 01-MAR-2002 (Rel. 41, created)
 DT 01-MAR-2002 (Rel. 41, last sequence update)
 DE Aurein 1.1.
 OS Litoria raniformis (Southern bell frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Litoria
 RN NCBI_TAXID=116057;
 RP [1]
 SEQUENCE AND FUNCTION.
 RC TISSUE=Granular dorsal gland;
 RX MEDLINE=20408845; PubMed=10951191;
 RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
 RA Wallace J.C., Tyler M.J.;
 RT "The antibiotic and anticancer active aurein peptides from the
 australian bell frogs *Litoria aurea* and *Litoria raniformis* the
 solution structure of aurein 1.2.";
 RL Eur. J. Biochem. 267:5330-5341(2000).
 -!- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST *B. CEREUS*, *L. LACTIS*,
 CC L. INNOVIA AND *S. SUBTILIS*. PROBABLY ACTS BY DISTURBING MEMBRANE
 CC FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
 KW -!- SUBCELLULAR LOCATION: SECRETED.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1447 MW; 173CB99DFBC83330 CRC64;

Query Match 18.4%; Score 25; DB 1; Length 13;
 Best Local Similarity 44.4%; Pred. No. 9et02; 1; Indels 0; Gaps 0;
 Matches 4; Conservative 4; Mismatches 1; Delins 0; Gaps 0;

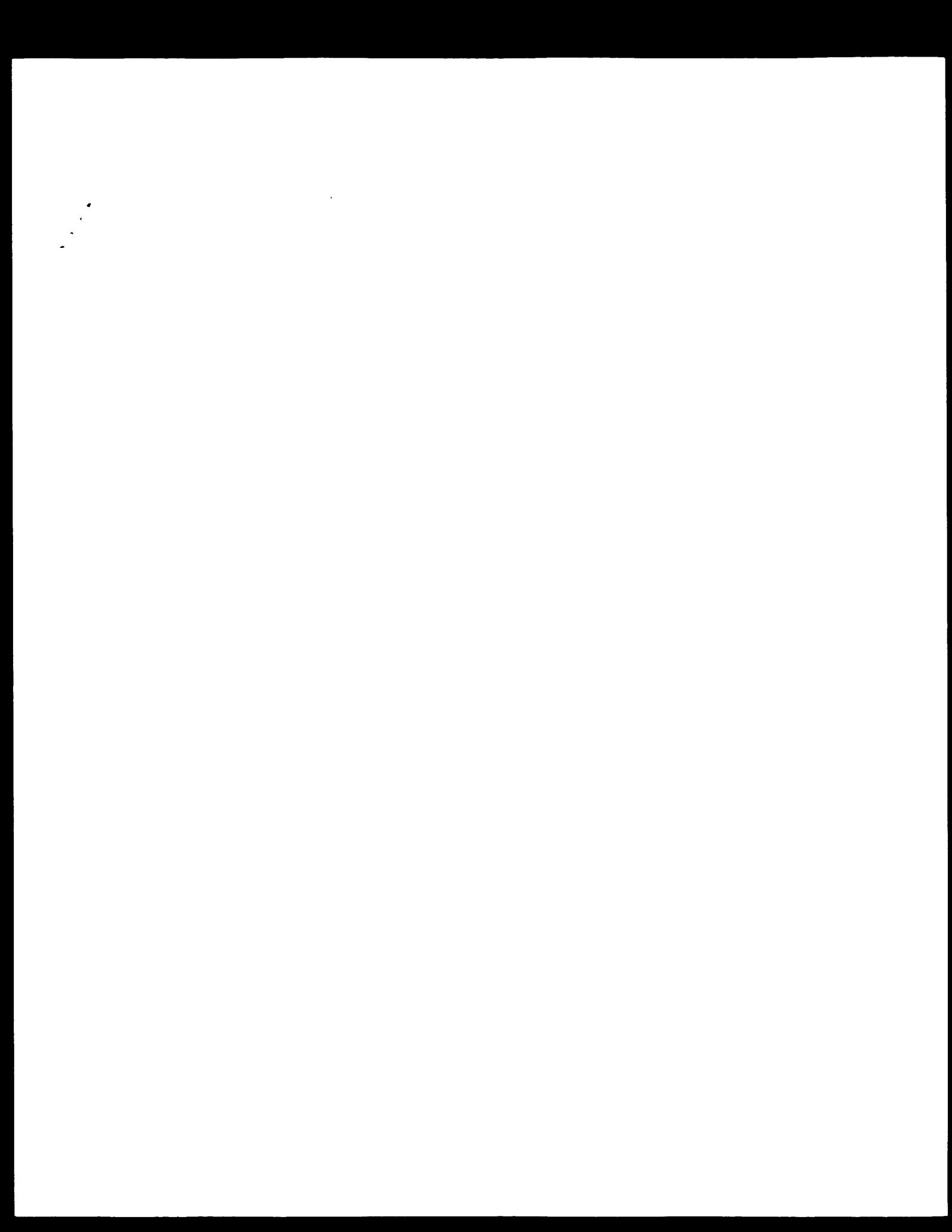
RESULT 15
 ID MC2_RHOOP STANDARD; PRT; 15 AA.
 AC P56870;
 DT 30-MAY-2000 (Rel. 39, created)
 DT 30-MAY-2000 (Rel. 39, last sequence update)
 DE Putative maleylacetate reductase II (EC 1.3.1.32) (Fragment).
 OS Rhodococcus Opacus (Nocardia opaca);
 OC Bacteria; Firmicutes; Actinobacteridae; Actinomycetales;
 OC Actinomycetales; Corynebacteriaceae; Nocardiaceae; Rhodococcus.
 RN NCBI_TAXID=37919;
 RP [1]
 SEQUENCE.
 RC STRAIN=ICP;
 RX MEDLINE=98324954; PubMed=9657989;
 RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
 CC "Characterization of a maleylacetate reductase encoding region from
 RT Rhodococcus opacus ICP".
 RL J. Bacteriol. 180:3503-3508(1998).
 CC -!- CATALYTIC ACTIVITY: 3-oxoadipate + NAD(P)(+)= 2-maleylacetate +
 CC NAD(P)H.
 CC -!- PATHWAY: 3-CHLOROCATECHOL DEGRADATION (BETA-KETOADIPIATE PATHWAY).
 CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
 CC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
 CC PRODUCTS AND AS INDUSTRIAL EFFLUENT.
 CC -!- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 DR InterPro: IPRE01670; FE-ADH.
 DR PROSITE: PS00913; ADH_IRON_1; PARTIAL.
 DR PROSITE: PS00060; ADH_IRON_2; PARTIAL.
 KW Aromatic hydrocarbons catabolism; oxidoreductase; NAD.
 FT NON_TER 15 15 15 AMIDATION.
 SQ SEQUENCE 15 AA; 1884 MW; 5DA90DD38F025E CRC64;

Query Match 18.4%; Score 25; DB 1; Length 15;
 Best Local Similarity 45.5%; Pred. No. 1et03; 1; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 4; Delins 0; Gaps 0;

QY 2 RYTHIPIPKDI 12
 | : | : |
 DB 2 RFEHENLQRI 12

RC TISSUE=Granular dorsal gland;
 RX MEDLINE=20408845; PubMed=10951191;
 RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
 RA Wallace J.C., Tyler M.J.;
 RT "The antibiotic and anticancer active aurein peptides from the
 australian bell frogs *Litoria aurea* and *Litoria raniformis* the
 solution structure of aurein 1.2.";
 RL Eur. J. Biochem. 267:5330-5341(2000).
 -!- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST *B. CEREUS*, *L. LACTIS*,
 CC L. INNOVIA, *M. LUPENS*, *P. MULTOCIDA*, *S. AREUS*, *S. EPIDERMIDIS* AND
 CC *S. UBERIS*. PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS

Search completed: July 15, 2002, 12:53:59
 Job time: 195 sec



DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
DE	TAT PROTEIN (FRAGMENT).	OX	NCBI_TaxID=4113;
GN		RN	[1]
OS	Human immunodeficiency virus type 1	RP	SEQUENCE.
OC	VIRUSES; Retroviridae; Lentivirus.	RX	MEDLINE=96198758; PubMed=7764624;
OX	NCBI_TaxID=11676;	RA	Braun H.P.; Krafft V.; Schmitz U.K.;
RN		RL	Planta 193:99-106(1994).
RC	SEQUENCE FROM N.A.	SQ	SEQUENCE 16 AA; (1946 MW; BBC625F8E4A4C8E7 CRC64;
STRA19-GCG12;			
RA	Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I., Harada Y.,		
RA	Hayami M., Ichimura H., Parra J.H.; "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in Republic of Congo-Brazzaville".		
RT	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AF127545; AAK64896.1; -.		
DR			
FT	NON_TER 19 19 SQ SEQUENCE 19 AA; 2210 MW; 2A83642B89068236 CRC64;		
FT			
Query Match	22.1%; Score 30; DB 15; Length 19;	RESULT	5
Best Local Similarity	53.8%; Pred. No. 1e+03; 0; Mismatches 6; Indels 0; Gaps 0;	ID	01271
Matches	7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	ID	016271
Qy	6 PHLPKDIVRSIAK 18	PRELIMINARY	PRELIMINARY;
Db	7 PHSSKDHNNSIPK 19	PRT	PRT; 19 AA.
RESULT	3		
Q99JY2			
TD	099JY2 PRELIMINARY; PRT; 20 AA.		
AC			
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	HYPOTHETICAL 2.2 KDA PROTEIN (FRAGMENT).		
OS	MUS musculus (mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Strasbourg R.; DR Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; BC005653; AAH05653.1; -.		
DR			
KW	Hypothetical protein.		
FT	NON_TER 1 SQ SEQUENCE 20 AA; 2223 MW; F203F6A80A7A0429 CRC64;		
FT			
Query Match	22.1%; Score 30; DB 11; Length 20;	Query Match	21.3%; Score 29; DB 4; Length 19;
Best Local Similarity	70.0%; Pred. No. 1.1e+03; 0; Mismatches 3; Indels 0; Gaps 0;	Best Local Similarity	37.5%; Pred. No. 1.5e+03; 2; Mismatches 8; Indels 0; Gaps 0;
Matches	7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Matches	6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
Qy	13 VRSTIAKAPK 22	RESULT	6
Db	1 VFSAAKRPK 10	ID	Q9MX47
RESULT	4	PRELIMINARY	PRELIMINARY;
Q9T2R0	' PRELIMINARY; PRT; 16 AA.	PRT	PRT; 22 AA.
ID	Q9T2R0		
AC			
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 15, Last annotation update)		
DE	CYTOCHROME-C REDUCTASE 14 KDA SUBUNIT (EC 1.10.2.2) (FRAGMENT).		
OS	Solanum tuberosum (Potato).		
OG	Mitochondrion.		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
RA	Naruse K., Oku H., Kojima A., Bessho Y., Kuroda N., Matsuzaki T.,		

RA	Hori H., Shima A., Nonaka M.;	Molecular cloning and linkage analysis of medaka fish MHC class II B genes.",	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.	FT	NON_TER	15 AA;	15 MW;	4EDFDA937C826170 CRC64;
RT	"Molecular cloning and linkage analysis of medaka fish MHC class II B genes.",			RT	SEQUENCE	15 AA;	15 MW;	4EDFDA937C826170 CRC64;
RL				RL	Best Local Similarity	19.9%;	Score 27;	DB 4; Length 15;
DR				DR	Matches	4;	Pred. No. 2.3e+03;	
EMBL:	AB033316;	BA094203.1;	-.	EMBL:	Conservative	4;	Mismatches 1;	Indels 0;
FT	NON_TER	1	1	FT	Indels	0;	Gaps 0;	
FT	NON_TER	22	22	FT	Mismatches	5;	Pred. No. 2.4e+03;	
SEQUENCE	22 AA;	2441 MW;	E2AF1A9CD581P5FB CRC64;	SEQUENCE	Length	22;		
SQ				SQ	Score	28;	DB 7;	Best Local Similarity 38.5%;
Db				Db	DB	20.6%;	Length 22;	Best Local Similarity 38.5%;
Db				Db	DB	20.6%;	Length 22;	Best Local Similarity 38.5%;
Db				Db	DB	20.6%;	Length 22;	Best Local Similarity 38.5%;
RESULT	7			RESULT	7			RESULT
Q9J7NB				Q9J7NB				Q9J7NB
ID	Q9J7NB			ID	Q9J7NB			ID
AC	Q9J7NB;			AC	Q9J7NB;			AC
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			DT
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)			DT
DE	BMPD (FRAGMENT).			DE	MICRIN (FRAGMENT).			DE
GN				GN				GN
OS	Borrelia afzelii.			OS	Homo sapiens (Human).			OS
OC	Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.			OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OC
OX	NCBI_TaxID=29518;			OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			OX
RN	[1]			RN	[1]			RN
RP	SEQUENCE FROM N.A.			RP	SEQUENCE FROM N.A.			RP
RC	STRAIN=IP3;			RC	MEDLINE=89235154; PubMed=2715633;			RC
RX	MEDLINE=20179823; PubMed=10715014;			RX	Xing P.X., Tjandra J.J., Reynolds K., McLaughlin P.J., Purcell D.F.J.,			RX
RA	Gorbacheva V.Y., Godfrey H.P., Cabello F.C.;			RA	McKenzie I.F.C.,			RA
RT	"Analysis of the bmp-2 gene family in Borrelia burgdorferi sensu lato.";			RT	"reactivity of anti-human milk fat globule antibodies with synthetic			RT
RL	J. Bacteriol. 182:2037-2042(2000).			RL	peptides.", J. Immunol. 142:3503-3509(1989).			RL
DR	EMBL: AF222435; AAC45174.1; -.			DR	EMBL: M26316; AAA6335.1; -.			DR
FT	NON_TER	1	1	FT	NON_TER	20	20	FT
SQ	SEQUENCE 24 AA;	2681 MW;	57F3887CD59126F9 CRC64;	SQ	SEQUENCE 20 AA;	1887 MW;	5B3473EABAFA87 CRC64;	SQ
Query Match	20.6%;	Score 28;	DB 2;	Query Match	19.9%;	Score 27;	DB 4;	Query Match
Best Local Similarity	46.2%;	Pred. No. 2.6e+03;	Length 24;	Best Local Similarity	71.4%;	Pred. No. 3.1e+03;	Length 20;	Best Local Similarity
Matches	6;	Conservative	2;	Matches	5;	Conservative	0;	Matches
QY	12 IVRSIAKAPGKA 24			QY	19 APGKRAP 25			QY
DB	1 IINGILKIKAPYDKA 13			DB	6 APGSTAP 12			DB
RESULT	10			RESULT	10			RESULT
Q9N0J5				Q9N0J5				Q9N0J5
ID	Q9N0J5			ID	Q9N0J5			ID
AC	Q9N0J5;			AC	Q9N0J5;			AC
DT	01-OCT-2000 (TREMBLrel. 15, Created)			DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			DT
DT	01-OCT-2000 (TREMBLrel. 13, Last sequence update)			DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			DT
DE	CHOLINE ACETYLTRANSFERASE (FRAGMENT).			DE	CHOLINE ACETYLTRANSFERASE (FRAGMENT).			DE
GN				GN	CIIA1.			GN
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OS	Saguinus imparator (Tamarin).			OS
OC	Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.			OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OC
OX	NCBI_TaxID=9491;			OX	Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.			OX
RN	[1]			RN	[1]			RN
RP	SEQUENCE FROM N.A.			RP	SEQUENCE FROM N.A.			RP
RA	Maiti A.K., Mattei M.G., Jorissen M., Volz A., Ziegler A., Bouvagnet P.;			RA	Mubumbila M.V.			RA
RT	"Chromosomal localization of human dynein heavy chain genes."			RT	"ChAT gene evolution in the mammalian genome."			RT
RL	Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.			RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.			RL
DR	EMBL: AJ132092; CAA10565.1; -.			DR	EMBL: AJ276478; CAB77548.1; -.			DR
FT	NON_TER	1	1	FT	KW	Transferase.		FT
SQ	SEQUENCE 21 AA;	2255 MW;	CB5D0293BC3B05AF CRC64;	SQ	SEQUENCE 21 AA;	2255 MW;	CB5D0293BC3B05AF CRC64;	SQ
Query Match	19.9%;	Score 27;	DB 6;	Query Match	19.9%;	Score 27;	DB 6;	Query Match
Best Local Similarity	50.0%;	Pred. No. 2.6e+03;	Length 21;	Best Local Similarity	50.0%;	Pred. No. 2.6e+03;	Length 21;	Best Local Similarity
Matches	6;	Conservative	2;	Matches	5;	Conservative	0;	Matches

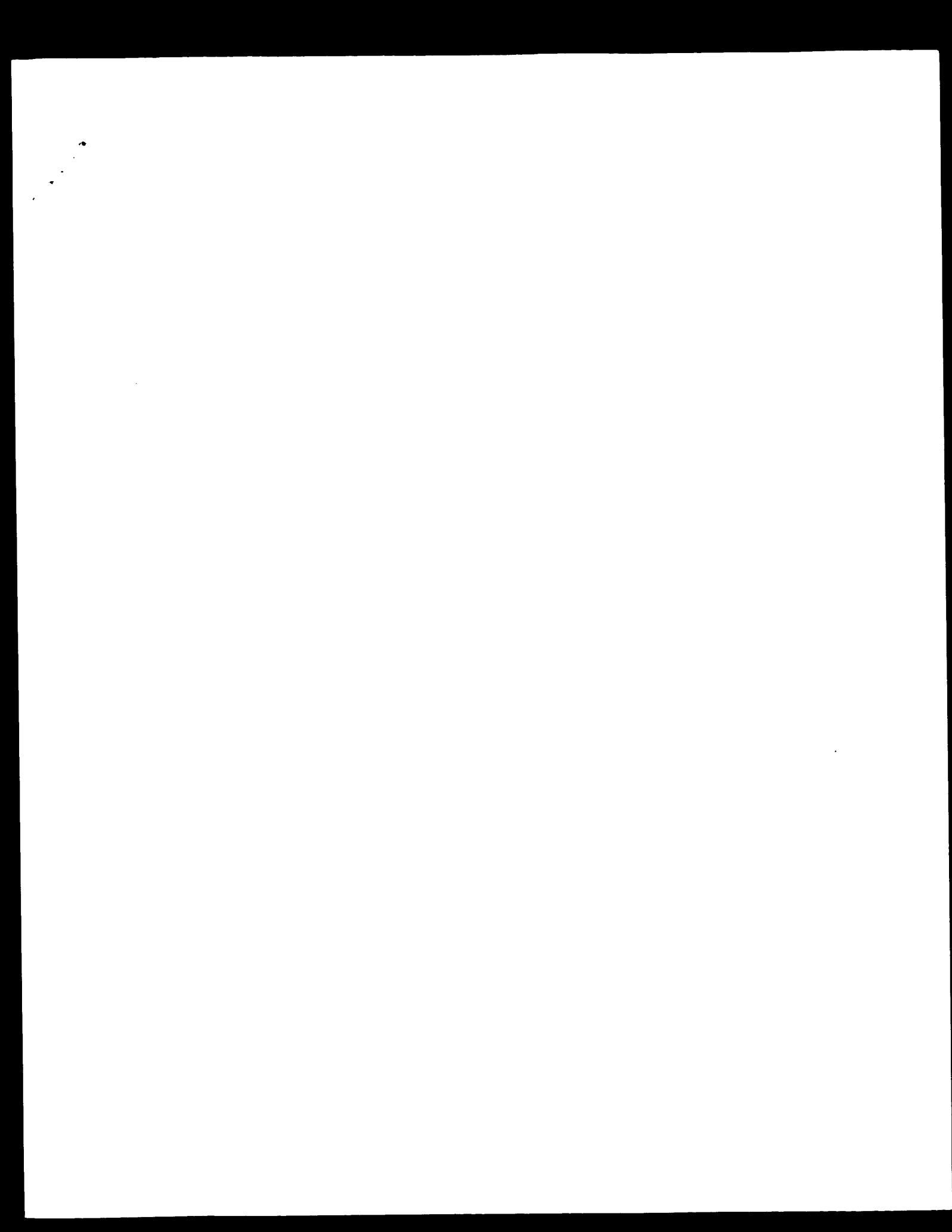
		Best Local Similarity 46.7%; Pred. No. 3.2e+03; Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;	AC Q9UCJB;
Qy	6	PHPLKDIYRSTAKAPR 20 ;	DT 01-MAY-2000 (TREMBLrel. 13, Created)
Db	2	PILGKDPHMAKTP 16	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
RESULT	11		DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
Q9TWR3		PRELIMINARY;	DE TYPE IV PROCOLLAGENASE (FRAGMENT).
ID	Q9TWR3	PRT; 17 AA.	OS Homo sapiens (Human)
AC	Q9TWR3:		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
DT	01-MAY-2000 (TREMBLrel. 13, Created)		OX NCBI_TaxID=9606;
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		RN [1]
DE	HISTONE H1 (FRAGMENT).		RP SEQUENCE.
OS	Trypanosoma cruzi.		RX MEDLINE=93125366; PubMed=1480041;
OC	Bukaryota; buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.		RA Stettler, Stevenson W.G., Krutzsch H.C., Liotta L.A.;
OX	NCBI_TaxID=5693;		RT "TIMP-2: identification and characterization of a new member of the metalloproteinase inhibitor family";
RN	[1]		RL Matrix Suppl. 1:299-306(1992);
RP	SEQUENCE.		SQ SEQUENCE 15 AA: 1537 MW; DSDAIAAA9C32276C CRC64;
RX	MEDLINE=94043510; PubMed=8227175;		
RA	Toro G.C., Galanti N., Hellman U., Wernstedt C.;		
RT	"Unambiguous identification of histone H1 in Trypanosoma cruzi.";		
RL	J. Cell. Biochem. 52:31-39 (1993).		
SQ	SEQUENCE 17 AA: 1820 MW; AD1BBC32D8ECD5 CRC64;		
Query Match	Best Local Similarity 40.0%; Score 26.5; DB 5; Length 17; Matches 6; Conservative 4; Mismatches 2; Indels 3; Gaps 1;	RESULT 12	AC Q9T2V8;
Qy	9	PKDIVRSIAKAPKR 23 ::	AC Q9T2V8;
Db	6	PK--KAVKKAKKK 17	PRELIMINARY; PRT; 22 AA.
RESULT	12		DT 01-MAY-2000 (TREMBLrel. 13, Created)
Q9SBB			DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
ID	Q9SBB		DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
AC	Q9SBB;	PRELIMINARY; PRT; 22 AA.	DB 2-ENOYL-COA HYDRATASE (FRAGMENT).
DT	01-MAY-2000 (TREMBLrel. 13, Created)		OS Homo sapiens (Human).
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		OG Mitochondrion.
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE	POLYGLACURONASE HOMOLOG (FRAGMENT).		OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OS	Oenothera ornatissima (Evening primrose).		OX NCBI_TaxID=9606;
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicots; Rosidae; Ericales; Malpighiales; Myrtales; Onagraceae; Oenothera.		RN [1]
OC	Eukaryota; buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.		RP SEQUENCE FROM N.A.
OX	NCBI_TaxID=3945;		RX MEDLINE=93046184; PubMed=7958339;
RN	[1]		RA Middleton B.;
RP	SEQUENCE FROM N.A. MEDLINE=93005658; PubMed=2152116;		RT "The mitochondrial long-chain trifunctional enzyme: 2-enoyl-CoA hydratase, 3-hydroxyacyl-CoA dehydrogenase and 3-oxoacyl-CoA thiolase."; Blochian. Soc. Trans. 22:427-431(1994); 31AD66A30B0B019A CRC64;
RX	Brown S.M., Crouch M.L.;		SQ SEQUENCE 16 AA: 1763 MW; 31AD66A30B0B019A CRC64;
RA	"Characterization of a gene family abundantly expressed in Oenothera organensis pollen that shows sequence similarity to polygalacturonase.";		
RT	Plant Cell 2:265-274(1990);		
RL	SEQUENCE 22 AA: 2289 MW; 2383FFFBALF3CCC70 CRC64;		
Query Match	Best Local Similarity 38.1%; Score 26.5; DB 10; Length 22; Matches 8; Conservative 3; Mismatches 9; Indels 1; Gaps 1;	RESULT 15	AC Q95JA2;
Qy	1	CRYTHHLKDIYRSTAKAPR 21 :	AC Q95JA2;
Db	1	CTITNAQL-FDIRTYGAKGDD 20	PRELIMINARY; PRT; 18 AA.
RESULT	13		DT 01-DEC-2001 (TREMBLrel. 19, Created)
Q9UCJB			DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
ID	Q9UCJB		DE INTEGRIN ALPHA 2 SUBUNIT (FRAGMENT).
PRELIMINARY; PRT; 15 AA.			OS Sus scrofa (Pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		OC NCBII_TaxID=9823;

[1]

RN
RP
SEQUENCE FROM N.A.
RC
TISSUE-CARDIOVASCULAR;
RA
Markmann A.; Kresse H.;
RT
"Regulation of VSMC Differentiation.",
RL
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR
EMBL; AF330200; AAL09466.1; ~
FT
NON_TER 1 1
FT
NON_TER 18 18
SQ
SEQUENCE ` 18 AA; 1944 MW; DFEA4C6E14A5E0EF CRC64;

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Best Local Similarity 50.0%; Pred No. 3 9e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0;
Gaps 0;
QY
9 PKDIVRSI 16
| | : | : |
Db 4 PSDWVNSL 11

Search completed: July 15, 2002, 12:53:42
Job time: 198 sec



Gencore version 4.5						
Copyright (c) 1993 - 2000 Compugen Ltd.						
OM protein - protein search, using sw model						
Run on: July 15, 2002, 12:45:19 ; Search time 30.15 Seconds						
Scoring table: BIOSUM62						
Gapop 10.0 , Gapext 0.5						
Searched: 74574 seqs, 111073796 residues						
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 45 summaries						
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
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1	136	100.0	124	18	AAW24097	Partial canine imm
2	136	100.0	312	21	AAV79995	Dog immunoglobulin
3	136	100.0	417	18	AAW23067	Canine IgE heavy c
4	136	100.0	426	17	AAR97753	Canine IgE. Canis
5	120.5	88.6	341	21	ABO6208	Immunogenic peptide
6	105	77.2	340	21	ABO3643	Rat IgE heavy chain
7	102	75.0	20	18	AAW4102	Canine immunoglob
8	99.5	73.2	341	21	ABO6206	Immunogenic peptide
9	95.5	70.2	342	21	ABO6205	Immunogenic peptide
10	93.5	68.8	345	21	ABO6207	Antibody 15A.2 bin
11	89	65.4	17	21	AY50893	
RESULT 1						
ID	AAW24097	standard; peptide; 124 AA.	XX	AAW24097;	XX	
AC			XX	AAW24097;	XX	
DT	21-NOV-1997	(first entry)	XX			
DE	Partial canine immunoglobulin E protein.	XX				
KW	Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.	XX				
OS	Canis familiaris.	OS				
PN	JPP0169795.A.	XX				
PD	30-JUN-1997.	XX				
PF	22-DEC-1995;	95JP-0334381.	PF			
PR	22-DEC-1995;	95JP-0334381.	PR			
PA	(HITB) HITACHI CHEM CO LTD.	PA				
XX	WPI: 1997-389423/36.	XX				
DR	N-FSDB; AAT85646.	DR				
CC	This is a partial canine immunoglobulin E (IgE) protein. Peptide fragments (AAW24097-106) containing at least five continuous amino acids	CC				

CC of this sequence are used for the preparation of anti-canine IgE
 CC antibody. The anti-canine IgE antibody can be used for the diagnosis of
 CC canine allergies.
 XX sequence.

Query Match 100.0%; Score 136; DB 18; Length 124;
 Best Local Similarity 100.0%; Pred. No. 2.6e-13; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; AC AAW23087;
 Qy 1 CRYMPHILPKDIVRSIAKPGKRAP 25
 Db 62 crvthphlpkdivrsiakpgkrap 86

RESULT 2
 AAY79995 standard; Protein; 312 AA.
 XX
 AC AAY79995;
 XX
 DT 15-MAY-2000 (first entry)
 XX
 DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
 XX
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis;
 XX
 OS Canis sp.
 XX
 PN W09867283-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13959.
 XX
 PR 20-JUN-1998; 98US-0100287.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY, Walfield AM;
 DR WPI; 2000-160578/14.
 XX
 PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunisation against allergy -
 XX
 PS Example 1; Page 66-68; 15pp; English.

The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 dermatitis. Nucleic acids that encode these compounds are useful for
 recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX Sequence 312 AA;

Query Match 100.0%; Score 136; DB 21; Length 312;
 Best Local Similarity 100.0%; Pred. No. 7.4e-13; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; AC AAW23067;
 Qy 1 CRYMPHIERFDVRSIAKARGKRAP 25
 Db 192 crvthphlpkdivrsiakpgkrap 216

RESULT 3
 AAY79995 standard; protein; 417 AA.
 XX
 AC AAW23067;
 XX
 DT 19-FEB-1998 (first entry)
 XX
 DE Canine IgE heavy chain constant region (exon 1-4 product).
 XX
 KW IgE; immunoglobulin; antibody; heavy chain constant region;
 KW allergy; hypersensitivity; therapy; dog; antisense;
 XX
 OS Canis familiaris.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 55
 FT /note= "encoded by ACC"
 FT Misc-difference 56
 FT /note= "encoded by TAC"
 FT Misc-difference 67
 FT /note= "encoded by GCC"
 FT Misc-difference 83
 FT /note= "encoded by NNT"
 FT Misc-difference 174
 FT /note= "encoded by GGN"
 FT Misc-difference 175
 FT /note= "encoded by NNG"
 FT Misc-difference 176
 FT /note= "encoded by TGN"
 FT Misc-difference 203
 FT /note= "encoded by TCC"
 FT Misc-difference 204
 FT /note= "encoded by GAC"
 XX
 PN W09730156-A2.
 XX
 PD 21-AUG-1997.
 XX
 PF 14-FEB-1997; 97WO-US02322.
 XX
 PR 14-FEB-1996; 96US-0601197.
 XX
 PA (INDEX-) IDEXX LAB INC.
 XX
 PI Harris RA, Mermel B, Siefring AE;
 XX
 DR WPI; 1997-425031/39.
 XX
 PS N-PDB; AAT79278.

PT Isolated canine IgE heavy chain constant region DNA - useful to
 PT develop products for treatment of canine allergies and for
 PT immunomodulation in dogs
 XX
 DR
 PS Disclosure; Page 35-39; 59pp; English.

CC This polypeptide is encoded by exons 1-4 (see AAT79278) of canine
 CC IgE heavy chain constant region (epsilon) genomic DNA. Another
 CC polypeptide, comprising the exon 5 and 6 product, is given in
 CC AAW23068. Recombinant peptides encoded by exons 1-6 can be
 CC produced in eukaryotic or prokaryotic cells. Such peptides,
 CC and the antibodies raised against them, are used in methods to treat
 the manifestation of allergy in dogs, e.g. to treatment Type I

PD 11-MAY-2000.
 XX
 PF 21-OCT-1999; 99WO-SE01896.
 XX
 PR 02-NOV-1998; 98US-0106652.
 PR 22-SEP-1999; 99US-0401636.
 PA (RESI-) RESIDENTIA PHARM AB.
 XX
 PT Hellman LT;
 XX
 DR WPI; 2000-365342/31.
 XX
 PT Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals - Disclosure; Fig 1; 50pp; English.
 XX
 CC The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2, 3 and 4 of the rat IgE. It was used to construct a number of immunogenic peptides which consisted of regions of IgE from different mammals, which appear to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.
 CC Sequence 340 AA;

Query Match 77.2%; Score 105; DB 21; Length 340;
 Best Local Similarity 79.2%; Pred. No. 5.1e-08;
 Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 CRVTHPHPLPKDVRSTAKA 24
 CC ||||| ||||| ||||| |||||:
 Db 200 crvdphphpkpivrsitkapgrs 23

RESULT 7
 AAW24102
 TD AAW24102 standard; peptide; 20 AA.
 XX
 AC AAW24102;
 XX
 DT 21-NOV-1997 (first entry)
 XX
 DE Canine immunoglobulin E peptide 5.
 DE
 XX
 KW Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.
 XX
 OS Canis familiaris.
 XX
 PN JF09169795-A.
 XX
 PD 30-JUN-1997.
 XX
 PF 22-DEC-1995; 95JP-0334381.
 XX
 PR 22-DEC-1995; 95JP-0334381.
 PA (HITB) HITACHI CHEM CO LTD.
 XX
 DR WPI; 1997-38942/36.
 DR N-PSDB; AAT85651.

Query Match 73.2%; Score 99.5%; DB 21; Length 341;
 Best Local Similarity 76.9%; Pred. No. 3.7e-07;
 Matches 20; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 PS Disclosure; Fig 2; 50pp; English.
 XX
 CC The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the rat. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.
 CC Sequence 341 AA;

Query Match 75.0%; Score 102; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.1e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CRVTHPHPLPKDVRSTAKA 19
 CC ||||| ||||| |||||:
 Db 2 crvthphplkdvrsvika 20

RESULT 8
 AR06206
 ID AR06206 standard; protein; 341 AA.
 XX
 AC AR06206;
 XX
 DT 22-Nov-2000 (first entry)
 XX
 DE Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4.
 XX
 KW Rat; opossum; immunoglobulin E; IgE; vaccination; infection; allergy; asthma; eczema; immunogenic peptide.
 XX
 OS Chimeric - Didelphis virginiana.
 OS Chimeric - Rattus sp.
 XX
 PN WO200025722-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 21-OCT-1999; 99WO-SE01896.
 XX
 PR 02-NOV-1998; 98US-0106652.
 PR 22-SEP-1999; 99US-0401636.
 PA (RESI-) RESIDENTIA PHARM AB.
 XX
 PT Hellman LT;
 XX
 DR WPI; 2000-365342/31.

Query Match 75.0%; Score 102; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.1e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PS Disclosure; Fig 2; 50pp; English.
 XX
 CC The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the rat. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.
 CC Sequence 341 AA;

Query Match 73.2%; Score 99.5%; DB 21; Length 341;
 Best Local Similarity 76.9%; Pred. No. 3.7e-07;
 Matches 20; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 PS Disclosure; Fig 2; 50pp; English.
 XX
 PN AAW24098-106 are peptide fragments containing at least 5 continuous

XX
PS Disclosure; Fig 6; 30pp; English.

XX
CC This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy. AAY5086-5090 represent peptide mimotopes used in the method of the invention.

XX
SQ Sequence 17 AA;

Query Match

65.4%

Score 89;

DB 21;

Length 17;

Best Local Similarity 100.0%;

Pred. No. 5.2e-07;

Mismatches 0;

Indels 0;

Gaps 0;

Matches 16;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Qy 1 CRYTHPHLPKDIVSI 16

Db 2 crythphlpkdivsi 17

Query Match 65.4%; Score 89; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13

AAY7999 standard; Peptide; 25 AA.

ID AAY7999

AC AAY7999;

XX DT 15-MAY-2000 (first entry)

XX DE Optimised IgE-CH3 domain antigen peptide for dog IgE.

XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; epitope; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Canis sp.

XX PN Synthetic.

XX WO9967793-A1.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.

XX PA (UHBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfield AM;

XX DR WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy -

PT

XX PS Claim 1; Page 99; 15pp; English.

XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon heavy chain of IgE and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation, or for passive immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse sublectins), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactoenic) antibodies. AAY994 to AAY8084 represent amino acid sequences used in the exemplification of the present invention.

XX SQ Sequence 25 AA;

Query Match 65.4%; Score 89; DB 21; Length 25;

Best Local Similarity 100.0%; Pred. No. 8e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RVTHPHLPKDIVSI 18

XX
PS Binding proteins used for treatment or prophylaxis of canine allergy - disclosure; Fig 7; 30pp; English.

CC This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy. AAY5086-5090 represent peptide mimotopes used in the method of the invention.

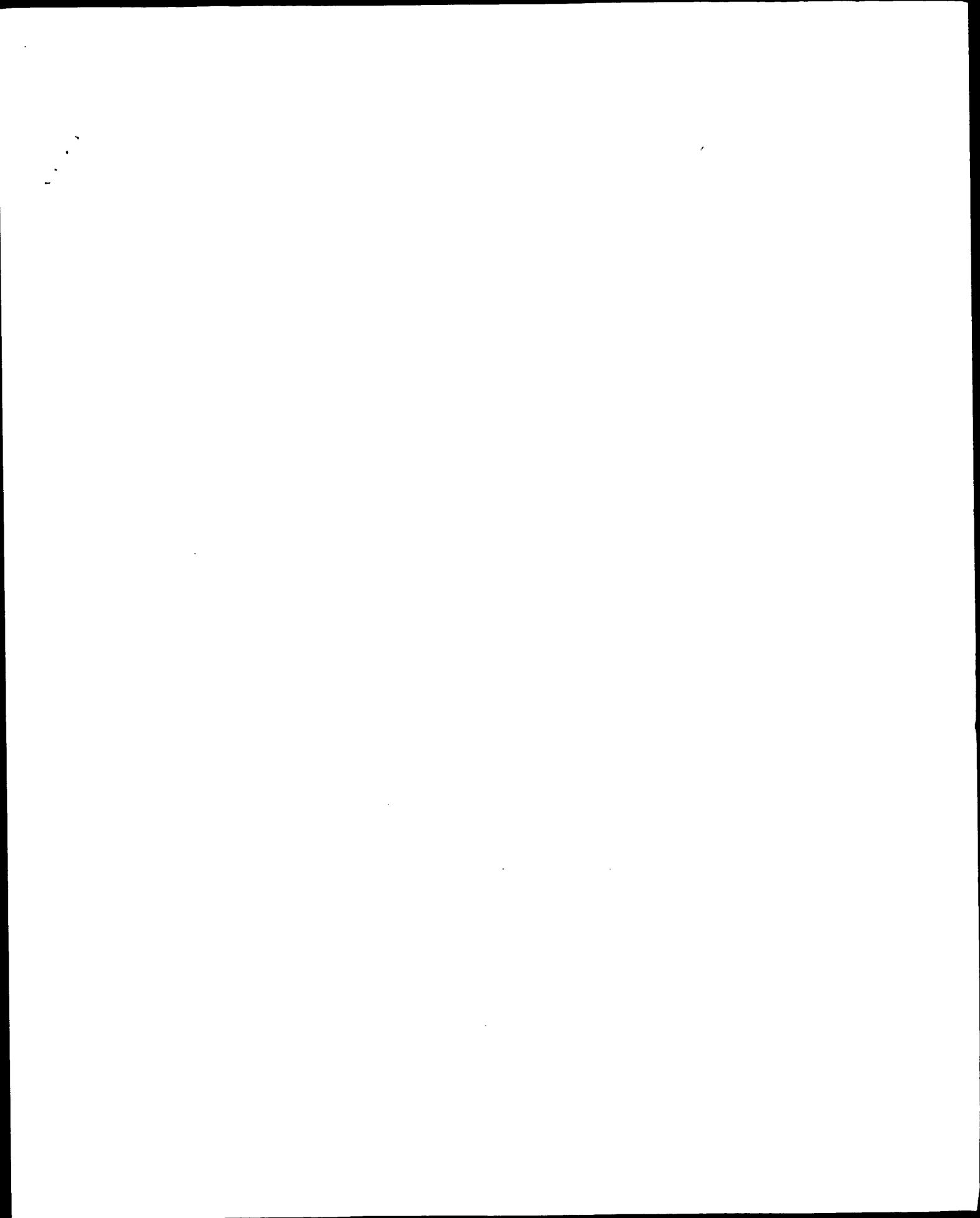
CC
SQ Sequence 17 AA;

Query Match 65.4%; Score 89; DB 21; Length 25;

Best Local Similarity 100.0%; Pred. No. 8e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RVTHPHLPKDIVSI 18



Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5
Run on:	July 15, 2002, 12:45:19 ; Search time 12.97 Seconds
OM protein - protein search, using sw model	47.081 Million cell updates/sec
Title:	US-09-938-700-4
Perfect score:	136
Sequence:	1 CRYTHPHLPKDIVRSIAKAPGKRAP 25
Scoring table:	BLOSUM62
Gapop 10.0 , Gapext 0.5	
Searched:	231628 seqs, 2425594 residues
Total number of hits satisfying chosen parameters:	231628
Minimum DB seq length: 0	
Maximum DB seq length: 200000000	
Post-processing: Minimum Match 0%	
Maximum Match 100%	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
Result No.	Score
	Match Length DB ID
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2	136 100.0
3	78 57.4
4	78 57.4
5	78 57.4
6	67.5 49.6
7	67.5 49.6
8	64 47.1
9	64 47.1
10	64 47.1
11	64 47.1
12	64 47.1
13	64 47.1
14	64 47.1
15	64 47.1
16	64 47.1
17	64 47.1
18	64 46.3
19	64 47.1
20	64 47.1
21	64 47.1
22	64 47.1
23	64 47.1
24	60 44.1
25	60 44.1
26	60 44.1
27	58 42.6
231	2 331
2	US-08-646-981-17
ALIGNMENTS	
RESULT 1	US-08-336-583-2
Sequence 2, Appli	Sequence 2, Application US/08336583
Patent No. 5626415	
GENERAL INFORMATION:	
APPLICANT: HOLLIIS, GREGORY F.	
APPLICANT: PATEL, MAYUR D.	
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E	
NUMBER OF SEQUENCES: 2	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: CHRISTINE E. CARTY	
STREET: 126 E. LINCOLN AVENUE	
CITY: RAILWAY	
STATE: NEW JERSEY	
ZIP: 07065-0300	
COMPONENTS:	
COMPUTER READABLE FORM:	
MEDIUM TYPE: Floppy disk	
COMPUTER: IBM PC compatible	
OPERATING SYSTEM: PC-DOS/MS-DOS	
SOFTWARE: PatentIn Release #1.0, Version #1.25	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/08-336,583	
FILING DATE: 09-NOV-1994	
CLASSIFICATION: 424	
ATTORNEY/AGENT INFORMATION:	
NAME: CARTY, CHRISTINE E.	
REGISTRATION NUMBER: 36,099	
REFERENCE/DOCKET NUMBER: 19211	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: (908) 594-6734	
TELEFAX: (908) 594-4720	
INFORMATION FOR SEQ ID NO: 2:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 426 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: protein	
US-08-336-583-2	
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Best Local Similarity	100.0%; Pred. No. 1 9e-13;
Matches	0; Mismatches 0; Indels 0; Gaps 0;
QV	1 CRYTHPHLPKDIVRSIAKAPGKRAP 25
Db	294 CRYTHPHLPKDIVRSIAKAPGKRAP 318

APPLICATION NUMBER: US/08/232,539D
 FILING DATE: 21-APR-1994
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/179583
 FILING DATE: 07-JAN-1994
 APPLICANT NUMBER: 07/744768
 FILING DATE: 14-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39,044
 REFERENCE/DOCKET NUMBER: P0718P3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1489
 TELEFAX: 650/932-9881
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 106 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-232,539D-54

Query Match 57.4%; Score 78; DB 2; Length 106;
 Best Local Similarity 61.9%; Pred. No. 4.3e-05; Mismatches 5; Indels 0; Gaps 0;
 Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CRYTHPHLPDIIVRSIAKPG 25
 Db 294 CRYTHPHLPDIIVRSIAKPG 318

RESULT 4
 US-08-466-163B-1
 Sequence 1, Application US/08466163B
 ; GENERAL INFORMATION:
 ; APPLICANT: Jardieu, Paula M.
 ; TITLE OF INVENTION: Immunoglobulin Variants
 ; FILE REFERENCE: P0718PCID1
 ; CURRENT APPLICATION NUMBER: US/08/466,163B
 ; CURRENT FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: US 08/405,617
 ; PRIOR FILING DATE: 1995-03-15
 ; PRIOR APPLICATION NUMBER: US 08/185,899
 ; PRIOR FILING DATE: 1994-01-26
 ; PRIOR APPLICATION NUMBER: US 07/879,495
 ; PRIOR FILING DATE: 1992-05-07
 ; PRIOR APPLICATION NUMBER: US 07/744,768
 ; PRIOR FILING DATE: 1991-08-14
 ; NUMBER OF SEQ ID NOS: 64
 ; SEQ ID NO 1
 ; LENGTH: 109
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 57.4%; Score 78; DB 4; Length 109;
 Best Local Similarity 61.9%; Pred. No. 4.3e-05; Mismatches 5; Indels 0; Gaps 0;
 Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CRYTHPHLPDIIVRSIAKPG 21
 Db 88 CRYTHPHLPRLMSTTKTG 108

RESULT 5
 US-08-232,539D-55
 Sequence 56, Application US/0823239D
 ; Patent No. 5965709

GENERAL INFORMATION:
 ; Patent No. 5965709
 ; APPLICANT: Presta, Leonard G.
 ; ATTORNEY/AGENT INFORMATION:
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: IgE Antagonists
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:

REGISTRATION NUMBER: 29,323
 REFERENCE/DOCKET NUMBER: 1111-4157

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 98:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-100-414B-98

Query Match Similarity 47.1%; Score 64; DB 3; Length 42;
 Best Local Similarity 64.7%; Pred. No. 0.0023; Matches 11; Conservatve 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLKDIVRSIAK 18
 Db 25 RVTHPHLPLRMLRSTK 41

RESULT 11

US-09-100-414B-99

Sequence 99, Application US/09100414B

PATENT No. 6023468

;

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: NOVEL LHRH PEPTIDE

TITLE OF INVENTION: IMMUNOGENS

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/100,414B

FILING DATE: 20-JUNE-1998

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1111-4157

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-100-414B-99

RESULT 12

US-09-100-414B-100

Sequence 98, Application US/09100414B

PATENT No. 6023468

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: NOVEL LHRH PEPTIDE

TITLE OF INVENTION: IMMUNOGENS

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/100,414B

FILING DATE: 20-JUNE-1998

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1111-4157

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-100-414B-100

Query Match Similarity 47.1%; Score 64; DB 3; Length 42;

Best Local Similarity 64.7%; Pred. No. 0.0023; Matches 11; Conservatve 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLKDIVRSIAK 18
 Db 25 RVTHPHLPLRMLRSTK 41

RESULT 13

US-09-03-323-98

Sequence 98, Application US/09303323

PATENT No. 622887

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: NOVEL LHRH PEPTIDE

TITLE OF INVENTION: IMMUNOGENS

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/303,323

FILING DATE: 30-APR-1999
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/100,414
 FILING DATE: 20-JUNE-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Maria H. Lin
 REGISTRATION NUMBER: 29,323
 REFERENCE/DOCKET NUMBER: 1151-4157
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-758-4800
 TELEFAX: 212-751-6849
 INFORMATION FOR SEQ ID NO: 98:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-303-323-98

Query Match Best Local Similarity 47.1%; Score 64; DB 4; Length 42;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 RVTHPHLPKDIVRSIAK 18
 Db 25 RVTHPHLPALMRSTIK 41

RESULT 14
 US-09-303-323-99
 Sequence 99, Application US/09303323
 ; Patent No. 6228987
 GENERAL INFORMATION:
 APPLICANT: Wang, Chang Yi
 TITLE OF INVENTION: NOVEL LHRH PEPTIDE
 TITLE OF INVENTION: IMMUNOGENS
 TITLE OF INVENTION: NOVEL LHRH PEPTIDE
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan & Finnegan, L.L.P.
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10154-0054
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC Windows
 SOFTWARE: Word 97
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/100,414
 FILING DATE: 20-JUNE-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Maria H. Lin
 REGISTRATION NUMBER: 29,323
 REFERENCE/DOCKET NUMBER: 1151-4157
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-758-4800
 TELEFAX: 212-751-6849
 INFORMATION FOR SEQ ID NO: 100:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-303-323-100

Query Match Best Local Similarity 64.7%; Score 64; DB 4; Length 42;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 RVTHPHLPKDIVRSIAK 18
 Db 25 RVTHPHLPALMRSTIK 41

RESULT 15
 US-09-303-323-100
 Sequence 100, Application US/09303323
 ; Patent No. 6228987
 GENERAL INFORMATION:
 APPLICANT: Wang, Chang Yi
 TITLE OF INVENTION: IMMUNOGENS
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan & Finnegan, L.L.P.
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10154-0054
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC Windows
 SOFTWARE: Word 97
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/303,323
 FILING DATE: 30-APR-1999
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/100,414
 FILING DATE: 20-JUNE-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Maria H. Lin
 REGISTRATION NUMBER: 29,323
 REFERENCE/DOCKET NUMBER: 1151-4157
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-758-4800
 TELEFAX: 212-751-6849
 INFORMATION FOR SEQ ID NO: 100:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-303-323-100

Query Match Best Local Similarity 64.7%; Score 64; DB 4; Length 42;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 RVTHPHLPKDIVRSIAK 18
 Db 25 RVTHPHLPALMRSTIK 41

Search completed: July 15, 2002, 12:45:40
 Job time: 21 sec

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.

ATTORNEY/AGENT INFORMATION:

APPLICANT: Jardieu, Paula M.

TITLE OF INVENTION: IGE Antagonists

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232, 539D

FILING DATE: 21-APR-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/178583

FILING DATE: 07-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744768

FILING DATE: 14-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Svoboda, Craig G.

REGISTRATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: P0718P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1489

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

S-08-232-539D-56

RESULT 6

Sequence 1, Application US/0846151

PATENT NO. 6037453

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464, 025A

FILING DATE: 05-Jun-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Svoboda, Craig G.

REGISTRATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: P0718C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1489

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-466-151-1

RESULT 7

Query Match Score 78; DB 2; Length 113;

Best Local Similarity 61.9%; Pred. No. 4.7e-05;

Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

1 CRYTHPHLPKDI-VRSIKA[P]G 21

||| ||| : : || |

91 CRYTHPHLPKALMRSTKTSG 111

Query Match Score 67.5; DB 3; Length 118;

Best Local Similarity 59.1%; Pred. No. 0.0022;

Matches 13; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 CRYTHPHLPKDI-VRSIKA[P]G 21

||| ||| : : | | |

Db 96 CRYTHPHLPKALMRSTKTSG 117

US-08-464-025A-1

Query Match Score 67.5; DB 3; Length 118;

Best Local Similarity 59.1%; Pred. No. 0.0022;

Matches 13; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 CRYTHPHLPKDI-VRSIKA[P]G 21

||| ||| : : | | |

Db 96 CRYTHPHLPKALMRSTKTSG 117

GENERAL INFORMATION:

APPLICANT: Jardieu et al.

TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464, 025A

FILING DATE: 05-Jun-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Svoboda, Craig G.

REGISTRATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: P0718C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1489

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:

Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5			
Run on:	July 15, 2002, 12:45:19 ; Search time 15.25 Seconds (without alignments) 157.523 Million cell updates/sec			
Title:	US-09-938-700-4			
Perfect score:	135			
Sequence:	CRVTHPHLPKDVRSITAKAPGKRAP 25			
Scoring table:	BLOSUM2			
Searched:	Gapext 0.5			
Total number of hits satisfying chosen parameters:	283138			
Maximum DB seq length:	0			
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries			
Database :	PIR_71: 1: pir1: * 2: pir2: * 3: pir3: * 4: pir4: *			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description
1	105	77.2	429	Ig epsilon chain C
1	89	65.4	426	Ig epsilon-chain -
2	86	63.2	428	Ig EHRU
3	80	58.8	388	Ig EIMN
4	80	58.8	548	Ig epsilon chain C38864
5	80	58.8	2	Ig epsilon chain C3 regio
6	67	49.3	107	Ig epsilon chain C3 regio
7	67	49.3	107	Ig epsilon chain C3 regio
8	59	43.4	684	Ig epsilon chain C3 regio
9	58	42.6	549	Ig epsilon chain C3 regio
10	54	39.7	1938	Ig epsilon chain C3 regio
11	54	39.7	1939	Ig epsilon chain C3 regio
12	54	39.7	1939	Ig epsilon chain C3 regio
13	52	38.2	197	Ig epsilon chain C3 regio
14	51	37.5	2	Ig epsilon chain C3 regio
15	51	37.5	1938	Ig epsilon chain C3 regio
16	51	37.5	1940	Ig epsilon chain C3 regio
17	51	37.5	1940	Ig epsilon chain C3 regio
18	50.5	37.1	277	Ig epsilon chain C3 regio
19	50.5	37.1	147162	Ig epsilon chain C3 regio
20	50.5	37.1	147162	Ig epsilon chain C3 regio
21	50.5	37.1	147161	Ig epsilon chain C3 regio
22	50.5	37.1	328	Ig epsilon chain C3 regio
23	50.5	37.1	328	Ig epsilon chain C3 regio
24	50.5	37.1	328	Ig epsilon chain C3 regio
25	50.5	37.1	330	Ig epsilon chain C3 regio
26	50.5	37.1	399	Ig epsilon chain C3 regio
27	50.5	37.1	466	Ig epsilon chain C3 regio
28	50.5	37.1	538	Ig epsilon chain C3 regio
29	50.5	37.1	538	Ig epsilon chain C3 regio
ALIGNMENTS				
RESULT 1				
ERI				
Ig epsilon chain C region - rat				
C;Species: Rattus norvegicus (Norway rat)				
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999				
C;Accession: A93442; A90397; A02143				
R;Hellman, L.; Petterson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.				
Nucleic Acids Res. 10, 6011-6049, 1982				
A;Title: Structure and evolution of the heavy chain from rat immunoglobulin E.				
A;Reference number: A34442; MUID:83064537				
A;Accession: A93442				
A;Molecule type: mRNA				
A;Residues: 1-129 <HEL>				
A;Experimental source: strain LOU/c/wsl, immunocytoma IR2				
R;Kindsvogel, W.R.; Reedy, E.P.; Moore, J.M.; Faust Jr., C.H.				
DNA 1, 335-343, 1982				
A;Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction				
A;Reference number: A90937; MUID:83182019				
A;Contents: myeloma IR162				
A;Accession: A90937				
A;Molecule type: mRNA				
A;Residues: N-169-307, 'L', 309-342 <KIN>				
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology				
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F:19-80/Domain: immunoglobulin homology <IM1>				
F:19-80/Domain: immunoglobulin homology <IM2>				
F:22-3/291/Domain: immunoglobulin homology <IM3>				
F:327-398/Domain: immunoglobulin homology <IM4>				
F:46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status pred				
Query Match Score 77.2%; Length 429; Best Local Similarity 79.2%; Pred. No. 2.4e-07; Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;				
QY 1 CRVTHPHLPKDVRSITAKAPGKRA 24				
Db 289 CRVDPHPKPTVRSITAKPGKRS 312				
RESULT 2				
Ig gamma-4 chain C				
Ig gamma-4 chain C				
Ig gamma 3 chain C				
Ig epsilon-chain - chimpanzee (fragment)				
Ig epsilon-chain - chimpanzee (fragment)				
C;Species: Pan troglodytes (chimpanzee)				
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000				
C;Accession: A16948				
R;Sakoyama, Y.; Hong, K.				
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987				
A;Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orang				
A;Reference number: A16948; MUID: 87147196				

A; Accession:	I3648
A; Status:	preliminary; translated from GB/EMBL/DBJ
A; Molecular type:	DNA
A; Residues:	1-426 <RBS>
A; Cross-references:	GB:MT5398; NID:9176797; PIDN:AAA35416.1; PID:9176798
A; Introns:	103/1; 209/1; 317/1
C; Superfamily:	Immunoglobulin C region; immunoglobulin homology <IMM> F; 356-405/Domain: immunoglobulin homology <IMM>
Query Match	65.4%
Best Local Similarity	66.7%
Matches	16;
Conservative	2;
Mismatches	6;
Indels	0;
Gaps	0;
Oy	1
Db	297
CRVTHPHLPRDIVRSIAKPCRA	24
: :	320
RESULT	3
RRHU	
IG epsilon chain C region - human	
C; Species:	Homo sapiens (man)
C; Date:	31-Mar-1981 sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C; Accession:	A22771; A23195; PH114; A93491; A90824; A94418; B93933; S02430; A53116; C46
R; Flanagan, J.G.; Rabitts, T.H.	
EMBO J.	1; 655-660; 1982
A; Title:	The sequence of a human immunoglobulin epsilon heavy chain constant region gene
A; Reference number:	A22771; MUID:84236029
A; Accession:	R22771
A; Molecule type:	DNA
A; Residues:	1-428 <FLA>
A; Cross-references:	GB:L00022; GB:J00227; GB:v00555; NID:9185035
R; Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.	
A; Title:	Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudogene
A; Reference number:	A23195; MUID:84207910
A; Accession:	A23195
A; Molecule type:	DNA
A; Residues:	2-428 <IEDB>
A; Cross-references:	GB:J00222; NID:9184755
R; Zhang, K.; Saxon, A.; Max, E.E.	
J. Exp. Med.	176; 233-43; 1992
A; Title:	Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A; Reference number:	PH1214; MUID:92308839
A; Accession:	PH1214
A; Molecule type:	DNA
A; Residues:	320-428 <ZHA>
A; Cross-references:	EMBL:X03663; GB:S38660; NID:932987
R; Seno, M.; Kuroki, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugai, A.; Title:	Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon genes.
A; Reference number:	AU3491; MUID:83168897
A; Accession:	A93491
A; Molecule type:	mRNA
A; Residues:	1-428 <SER>
A; Cross-references:	GB:LU00222; GB:J00227; GB:v00555; NID:9185035
R; Seno, M.; Kuroki, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugai, A.; Note:	this sequence difference may be due to polymorphism
R; Benich, H.H.; Johansson, S.G.O.; Von Barth-Lindstrom, H.	
A; Title:	Duplication and deletion in the human immunoglobulin epsilon genes.
A; Reference number:	A90824; MUID:83001945
A; Accession:	A90824
A; Molecule type:	DNA
A; Residues:	1-358; L' 360-428 <MAX>
A; Cross-references:	GB:J00222; NID:9184755
R; Benich, H.H.; Johansson, S.G.O.; Von Barth-Lindstrom, H.	
A; Title:	Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A; Reference number:	A94418
A; Accession:	A94418
A; Molecule type:	protein
A; Residues:	' GAWL', 6, X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 12

R; Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, I.O.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
 A; Reference number: A93933; MUID:83065234

A; Molecular type: mRNA
 A; Residues: 1-40; 68-114; 427-428
 A; Cross-references: GB:L00022; NID:9185035
 R; Ireyana, S.
 FEBS Lett. 224, 306-310, 1987
 A; Title: Purification and characterization of a recombinant human IgE Fc-epsilon frag
 A; Reference number: S02438; MUID:88083554

A; Accession: S02438
 A; Status: nucleic acid sequence not shown
 A; Molecule type: mRNA
 A; Residues: 98-352 <IKE>
 R; Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
 J. Biol. Chem. 269, 456-462, 1994
 A; Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produ
 A; Reference number: A53116; MUID:94103254
 A; Accession: A53116
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 320-428 <2H2>
 A; Experimental source: myeloma U266-derived cell line AF-10
 R; Hellman, L.
 Eur. J. Immunol. 23, 159-167, 1993
 A; Title: Characterization of four novel epsilon chain mRNA and a comparative analysis
 A; Reference number: A46536; MUID:93122085

A; Accession: C46536
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 382-426 <HEL>
 A; Cross-references: GB:S55273; NID:9263168; PIDN:AAB24857.1; PID:9263167
 A; Experimental source: B cell myeloma U-266
 A; Note: sequence extracted from NCBI backbone (NCBIP:125297)
 A; Accession: D6536
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 382-391 <HR2>
 A; Cross-references: GB:S55273; NID:9263168; PIDN:AAB24858.1; PID:9263169
 A; Experimental source: B cell myeloma U-266
 A; Note: sequence extracted from NCBI backbone (NCBIP:125299)
 A; Accession: A46536
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: DNA
 A; Residues: 401-428 <IE3>
 A; Cross-references: GB:S55497; NID:9263162; PIDN:AAB24855.1; PID:9263163
 A; Experimental source: B cell myeloma U-266
 A; Note: sequence extracted from NCBI backbone (NCBIP:123483)
 C; Genetics:
 A; Gene: GBP; ID:HE
 A; Cross-references: GDB:119335; OMIM:147180
 A; Map position: 14q32.33-14q32.33
 A; Introns: 1/1; 10/1; 211/1; 319/1
 C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (l
 C; Superfamily: immunoglobulin C region; immunoglobulin homology
 C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl
 F:1-22-87-domain: immunoglobulin homology <IM1>
 F:1-128-195-domain: immunoglobulin homology <IM2>
 F:232-301-domain: immunoglobulin homology <IM3>
 F:338-407-domain: immunoglobulin homology <IM4>
 F:14-disulfide bonds: interchain (to light chain) #status predicted
 F:15-105-298-315-295-193-239-299-345-405-disulfide bonds: #status predicted
 F:21-49-99-146-252-275-binding site: carbohydrate (asn) (covalent) #status predicted
 F:1121-121-209-disulfide bonds: interchain (to heavy chain) #status predicted

RESULT 4

EMHS

19 epsilon chain C region (version 1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Accession: A02144

R;Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.

Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982

A;Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.

A;Reference number: A02144; MUID:8311774

A;Molecule type: mRNA

A;Residues: 1-388 <LIU>

A;Cross-references: GB:J00476; NID:9194875; PIDN:AAA38085.1; PID:939720

C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin homology

F;1-44/Domain: immunoglobulin homology (fragment) <IM1>

F;81-149/Domain: immunoglobulin homology <IM2>

F;186-234/Domain: immunoglobulin homology <IM3>

F;120-361/Domain: immunoglobulin homology <IM4>

F;10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match 58.8%; score 80; DB 1; length 388;

Best Local Similarity 62.5%; Pred. No. 0; 0.00088;

Matches 15; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDKIVRSIKAQKRA 24

Db 252 CIVDHPDPFPKPIVRSIKTPGQRS 275

RESULT 5

S38864

19 epsilon chain C region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001

C;Accession: S38864

R;Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A;Description: Combination of a defined specificity and desired isotype by cloning of an antibody.

A;Reference number: S38864

A;Accession: S38864

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-548 <KIP>

A;Cross-references: EMBL:Z27397; NID:9416537; PIDN:CAA81788.1; PID:940782

C;Superfamily: immunoglobulin C region; immunoglobulin homology <IM1>

Query Match 58.8%; score 80; DB 2; length 548;

Matches 15; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDKIVRSIKAQKRA 24

Db 419 CIVDHPDPFPKPIVRSIKTPGQRS 442

RESULT 6

168730

19B chain C3 region - mouse (fragment)

C;Species: Mus musculus (house mouse)

RESULT 7

168736

19E chain C3 region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C;Accession: I68726

R;Shinkai, Y.; Nakuchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acids of the immunoglobulin genes.

A;Reference number: 154443; MUID:83152907

A;Accession: I68726

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-107 <RES>

A;Cross-references: GB:M22930; NID:9194455; PIDN:AAA37911.1; PID:9194460

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;22-90/Domain: immunoglobulin homology <IM1>

RESULT 8

S60266

Query Match 49.3%; score 67; DB 2; length 107;

Best Local Similarity 65.0%; Pred. No. 0.018; 0.018;

Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDKIVRSIKAQ 20

Db 88 CIVDHPDPFPKPIVRSIKTP 107

Query Match 43.4%; score 59; DB 2; length 684;

Best Local Similarity 50.0%; Pred. No. 1.7; 1.7;

Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDKIVRSIKAQKRA 24

Db 419 CIVDHPDPFPKPIVRSIKTPGQRS 442

Query Match 43.4%; score 59; DB 2; length 684;

Best Local Similarity 50.0%; Pred. No. 1.7; 1.7;

Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDKIVRSIKAQKRA 24

Db 419 CIVDHPDPFPKPIVRSIKTPGQRS 442

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C;Accession: I68730

R;Shinkai, Y.; Nakuchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acids of the immunoglobulin genes.

A;Reference number: 154443; MUID:83152907

A;Accession: I68730

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Cross-references: GB:M22930; NID:9194455; PIDN:AAA37911.1; PID:9194460

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;22-90/Domain: immunoglobulin homology <IM1>

Qy 1 CRYTHPHLPKDIVRSTAKAPGK 22
 | :||| :||| :|||
 Db 645 CLVGHPSLNRDLIRSTNKSNGK 666

RESULT 9

Ig heavy chain precursor - African clawed frog (fragment)

C;Species: Xenopus laevis (African clawed frog)
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999
 C;Accession: S04845
 R;Authors: C.T.; Haire, R.N.; Litman, G.W.
 Nucleic Acids Res. 17, 5308, 1989
 A;Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin
 A;Accession: S04845; MUID:89345103
 A;Molecule type: mRNA
 A;Residues: 1-549 <AME>
 A;Cross-references: EMBL:X15114
 R;Litman, G.W.
 submitted to the EMBL Data Library, April 1989
 A;Reference number: S05695
 A;Accession: S05695
 A;Molecule type: mRNA
 A;Residues: 'UC', 3-308, 'H', 310-549 <LT>
 A;Cross-references: EMBL:X15114; NID:964799; PID:g763031
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: glycoprotein; heterotetramer; immunoglobulin
 F:26-109/Domain: immunoglobulin homology <IMM>
 F:281-294/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 58; DB 2; Length 549;
 Best Local Similarity 52.8%; Pred. No. 1.9;
 Matches 12; Conservative 3; Mismatches 6; Indels 2; Gaps 1;
 Qy 1 CRYTHPHLPKDIVRSTAKA--PG 21
 | :||| :||| :||| :|||
 Db 424 CKVVFHDLPSPIEKSIQKSODPG 446

RESULT 10

myosin alpha heavy chain, cardiac muscle [similarity] - rat

N;Alternate names: alpha-myosin heavy chain
 N;Contains: myosin Arpase (EC 3.6.1.32)
 C;Species: Rat/mouse myosin (Norway rat)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
 C;Accession: S07335; MUID:902988; I53305
 R;McNally, E.M.; Gianola, K.M.; Leinwand, L.A.
 Nucleic Acids Res. 17, 7527-7528, 1989
 A;Title: Complete nucleotide sequence of full length cDNA for rat alpha cardiac myosin
 A;Reference number: S06005; MUID:9016822
 A;Accession: S06005
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-1938 <MCN>
 A;Cross-references: EMBL:X15938; NID:956654; PIDN:CAA340641; PID:g5655
 R;McNally, E.M.; Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.
 J. Mol. Biol. 210, 605-671, 1989
 A;Title: Full-length rat alpha and beta cardiac myosin heavy chain sequences. Comparison
 A;Reference number: S07535; MUID:90133919
 A;Accession: S07535
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-1938 <MC2>
 R;Mahdavi, V.; Chambers, A.P.; Nadal-Ginard, B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 2626-2630, 1984
 A;Title: Cardiac alpha and beta myosin heavy chain genes are organized in tandem.
 A;Reference number: A20971; MUID:84194059
 A;Molecule type: protein
 A;Residues: 1-12, 'AP', 14-45, 'A', 47-50, 'AP', 53-81, 'E', 83-86, 'Q', 88-109, 111-133, 'H', 135-16

R;Mahdavi, V.; Persasamy, M.; Nadal-Ginard, B.
 Nature 297, 659-664, 1982
 A;Title: Molecular characterization of two myosin heavy chain genes expressed in the
 A;Reference number: A02988; MUID:82220036
 A;Accession: A02988
 A;Molecule type: mRNA
 A;Residues: 1512-1574, 'S', 1576-1721, 'N', 1723-1851, 'N', 1853-1869, 'N', 1871-1933, 'I', 193
 A;Note: there are 110 or more myosin heavy chain genes in the rat, at least two of which
 R;Mahdai, V.; Lompre, A.M.; Chambers, A.P.; Nadal-Ginard, B.
 Eur. Heart J. 5, 131-131, 1984
 A;Title: Cardiac myosin heavy chain isoform transitions during development and under
 A;Reference number: I53305; MUID:85179510
 A;Accession: I53305
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1872-1933, 'I', 1935-1938 <RES>
 A;Cross-references: GB:M32097; NID:g205596; PIDN:AAA41658.1; PID:g205597
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 C;Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl
 F:87-765/Region: myosin motor domain homology <MMOT>
 F:177-884/Region: nucleotide-binding motif A (P-loop)
 F:58-595/Region: actin binding #status predicted
 F:566-678/Region: actin binding #status predicted
 F:840-1338/Region: coiled coil #status predicted <COI>
 F:840-1280/Region: S2
 F:1281-1938/Region: light meromyosin
 F:128/Modified site: NG, NG,N6-trimethyllysine (Lys) #status predicted
 F:183/Binding site: ATP (Lys) #status predicted
 F:696,706/active site: Cys #status predicted

RESULT 11

myosin alpha heavy chain, cardiac muscle - human

N;Contains: myosin Arpase (EC 3.6.1.32)
 C;Species: Homo sapiens (man)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
 C;Accession: A46762; MUID:949354; S18830; B33835; B07858; A28908
 R;Matsushita, R.; Beisel, K.W.; Furutani, M.; Arai, S.; Takao, A.
 Ann. J. Med. Genet. 41, 537-547, 1991
 A;Title: Complete sequence of human cardiac alpha-myosin heavy chain gene and amino acid
 A;Reference number: A46762; MUID:92133665
 A;Accession: A46762
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-1939 <MAT>
 A;Cross-references: DDBJ:D00943; NID:9219523; PIDN:BAA00791.1; PID:g219524
 A;Accession: B46762
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-1461 <Ma2>
 R;Bpp, T.A.; Dixon, I.M.C.; Wang, H.Y.; Sole, M.J.; Liew, C.C.
 Genomics 18, 505-509, 1993
 A;Title: Structural organization of the human cardiac alpha-myosin heavy chain gene (1-1939 <EPP>)
 A;Cross-references: GB:Z20656; NID:9297023; PIDN:CAA79675.1; PID:g297024
 R;Brand, N.J.; Dashade, N.; Yacoub, M.; Barron, P.J.R.
 Bloch, Biophys. Rev. Commun. 179, 125-128, 1991
 A;Title: Determination of the 5' exon structure of the human cardiac alpha-myosin hea

A; Reference number: S18830; MUID:92028859
A; Accession: S18830
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-32 <BRA>
A; Cross-references: EMBL:X56181; NID:928318; PIDN:CAA39642.1; PID:928319
R; Imauchi-Takahara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.
A; Title: Characterization of human cardiac myosin heavy chain genes.
A; Reference number: A942244; MUID:89264452
A; Accession: B32562
A; Molecule type: DNA
A; Residues: 1-87; Q, 89-177, 1551-1732, 'E', 1734-1736, 'T', 1738-1762, 'D', 1764-1848 <YAL>
R; Yamuchi-Takahara, K.; Sole, M.J.; Liew, J.; Ing, D.; Eddy, R.; Shows, T.B.; Leinwand
A; Reference number: A94226
A; Contents: erratum
A; Accession: B33353
A; Molecule type: DNA
A; Residues: 1-87; Q, 89-177, 1551-1732, 'E', 1734-1736, 'T', 1738-1762, 'D', 1764-1939 <YAL>
R; Saez, L.J.; Gianola, K.M.; McNamee, E.M.; Feghali, R.; Eddy, R.; Shows, T.B.; Leinwand
A; Title: Human cardiac myosin heavy chain genes and their linkage in the genome.
A; Reference number: A93669; MUID:87260010
A; Accession: B27858
A; Molecule type: DNA
A; Residues: 1-3, 'S', 5-10, 'T', 12, 14-67 <SAE>
R; Kurabayashi, M.; Tsuchimochi, H.; Komuro, I.; Takaku, F.; Yazaki, Y.
J. Clin. Invest. 82, 524-531, 1988
A; Title: Molecular cloning and characterization of human cardiac alpha- and beta-form my
human atrium.
A; Reference number: A92770; MUID:88299163
A; Accession: A26908
A; Molecule type: mRNA
A; Residues: 1407-1532, 'N', 1534-1539, 'W', 1541-1576, 'NV', 1579-1704, 'EQ', 1707-1762, 'D', 1764
A; Cross-references: GDB:120214; OMIM:160710
A; Map position: 14q11.2-14q13
C; Superfamily: myosin heavy chain; myosin motor domain homology <MMOT>
C; Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methylate
F; 88-768/Domain: myosin motor domain homology <MMOT>
F; 1-18-185/Region: nucleotide-binding motif A (P-loop)
F; 549-586/Region: actin binding #status predicted
F; 657-679/Region: actin binding #status predicted
F; 841-1939/Region: coiled coil #status predicted <COI>
F; 841-1281/Region: S2
F; 282-1939/Region: light meromyosin
F; 7129/modified site: ATP (lys) #status predicted
F; 697, 707/Active site: Cys #status predicted

Query Match 39.7%; Score 54; DB 1; Length 1939;
Best Local Similarity 50.0%; Pred. No. 25; Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Db 665 RTTHPHFWRCILPNERKAPG 684

RESULT 13
BB319 hypothetical protein CC0564 [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C; Accession: BB319
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; Laub, M.T.; Debey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kobayashi, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4156-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:2117698; PMID:11255647
A; Accession: BB319
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-273 <STO>
A; Cross-references: GB:AE005673; NID:913421758; PIDN:AAK22550.1; GSDB:GN00148
A; Genetics:
A; Gene: CC0564

Query Match 38.2%; Score 52; DB 2; Length 273;
Best Local Similarity 40.6%; Pred. No. 5.8; Matches 13; Conservative 5; Mismatches 4; Indels 10; Gaps 2;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 2 RVTTHPHLPKDVTAKAPG 21
Db 665 RTTHPHFWRCILPNERKAPG 684

RESULT 14
T33963 hypothetical protein SC9C7.12 - Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
C; Accession: T33963
R; Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M
submitted to the EMBL Data Library, January 1999
A; Reference number: Z21551
A; Accession: T33963
A; Status: preliminary
A; Molecule type: DNA

A; Residues: 1-197 <SPE>
A; Cross-references: EMBL:AL035161; PIDN:CAA22724.1; GSPDB:GN00070; SCOECD:SC9C7.12
A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOECD:SC9C7.12

Query Match 37.5%; Score 51; DB 2; Length 197;
Best Local Similarity 42.9%; Pred. No. 6.8; Mismatches 6; Indels 0; Gaps 0;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 3 VTHPHPLPKDIVRSIKAPEGKR 23
: || | : ||::: ||:||
Db 177 LAHPALAQAAVRALARIPGQR 197

RESULT 15

BA6529

Ig Y heavy chain (7.8S) - duck chain

N; Alternative names: Ig gamma chain (7.8S)

C; Species: Anas platyrhynchos (domestic duck)

C; Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C; Accession: B46529; S20759

R; Magor, K.E.; Wair, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.

J; Immunol. 159, 2627-2633, 1992

A; Title: Structural relationship between the two IgY of the duck, Anas platyrhynchos: mc

A; Reference number: A46529; MUID:93017865

A; Accession: BA6529

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-572 <NM>

A; Cross-references: EMBL:X65219; NID:962442; PIDN:CAA46322.1; PID:962443

A; Experimental source: spleen

A; Note: sequence extracted from NCBI backbone (NCBIP:116127)

C; Superfamily: immunoglobulin C region; immunoglobulin homology

C; Keywords: immunoglobulin homology <IMM>

C; KeyWords: immunoglobulin homology <IMM>

F; 37-120/Domain: immunoglobulin homology <IMM>

Query Match 37.5%; Score 51; DB 2; Length 572;
Best Local Similarity 50.0%; Pred. No. 20; Mismatches 9; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CRYTHPHPLPKDIVRSIKAPEGK 22
: || | : ||||| ||
Db 442 CTVQHPLPVPLGKSIAKHAGK 463

Search completed: July 15, 2002, 12:46:39
Job time: 80 sec

Scoring table:		Alignments									
Searched:	105224 seqs., 38719550 residues	Alignments									
Total number of hits satisfying chosen parameters:	105224										
Minimum DB seq length:	0										
Maximum DB seq length:	2000000000										
Post-processing:	Minimum Match 0%										
Maximum Match 100%											
Listing first 45 summaries											
Database :	SwissProt_40;*										
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES											
Result No.	Score	Query Match Length	DB ID	Description	RESULT	1	EPC_RAT	STANDARD;	PRT;	429 AA.	
1	105	77.2	429	1 EPC_HUMAN	RP	SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).					
2	86	63.2	428	1 EPC_MOUSE	RP	MEDLINE-8312019, PubMed=6820340;					
3	80	58.8	421	1 EPC_MOUSE	RA	Kindsvoel W.R., Reedy E.P., Moore J.M., Faust C.H. Jr.; RT					
4	54	39.7	1938	1 MYH6_RAT	DT	"A cloned cDNA probe for rat immunoglobulin epsilon chain: DT					
5	54	39.7	1939	1 MYH6_HUMAN	DT	construction, identification, and DNA sequence."					
6	54	39.7	1939	1 MYH6_MESAU	DT	DE 15-JUL-1999 (Rel. 38, last annotation update)					
7	51	37.5	1938	1 MYH6_MOUSE	DE	DE 19 epsilon chain C region.					
8	51	37.5	1940	1 MYH3_RAT	OS	Rattus norvegicus (Rat).					
9	51	37.5	1940	1 MYH3_RAT	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;					
10	50.5	37.1	327	1 G6A_HUMAN	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;					
11	50.5	37.1	330	1 G6C_MOUSE	OK	NCBI-TaxID=10116;					
12	50.5	37.1	339	1 GCAM_MOUSE	RN	[1] SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).					
13	50	36.8	736	1 MYH7_RABIT	RP	SEQUENCE OF 168-342 FROM N.A.					
14	50	36.8	1934	1 MYH7_MESAU	RP	MEDLINE-8217457; PubMed=6803238;					
15	50	36.8	1935	1 MYH7_HUMAN	RA	Hellman L., Petterson U., Bennich H.; RT					
16	50	36.8	1935	1 MYH7_PIG	RT	"Characterization and molecular cloning of the mRNA for the heavy RT					
17	50	36.8	1935	1 MYH7 RAT	RT	(epsilon) chain of rat immunoglobulin E;"					
18	49.5	36.4	336	1 GCB_MOUSE	RL	Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268 (1982).					
19	49.5	36.4	374	1 SPOP_HUMAN	CC	CC					
20	49.5	36.4	405	1 GCBL_MOUSE	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration CC					
21	49	36.0	1937	1 MYB_HUMAN	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation - CC					
22	49	36.0	1938	1 MYB_CHICK	CC	the European Bioinformatics Institute. There are no restrictions on its CC					
23	49	36.0	1939	1 MYBL_HUMAN	CC	use by non-profit institutions as long as its content is in no way CC					
24	49	36.0	1939	1 MYH4_HUMAN	CC	modified and this statement is not removed. Usage by and for commercial CC					
25	49	36.0	1941	1 MYH2_HUMAN	CC	entities requires a license agreement (see http://www.isb.ch/announce/ CC					
26	48.5	35.7	329	1 GCC_RAT	CC	or send an email to license@ib-sib.ch).					
27	48.5	35.7	330	1 GCL_HUMAN	DR	EMBL; J00744; ARX41379; ALT_INIT.					
28	48	35.3	1936	1 Y167_HUMAN	DR	PTR; A02143; EHRT.					
29	48	35.3	1935	1 MSS_CYPCA	DR	DR HSSP; P01854; IIGE.					
30	47	34.6	368	1 LNK_RAT	DR	DR InterPro; IPR03006; Ig-MHC.					
31	47	34.6	384	1 GBAL_LACES	DR	DR InterPro; IPR03597; Ig-cl.					
32	47	34.6	392	1 CAR5_RHINT	DR	DR Pfam; PF00047; Ig; 4.					
33	47	34.6	416	1 MKR2_HUMAN	DR	DR SMART; SM00410; Ig-like; 3.					
					DR SMART; SM00407; IgCl; 1.						
					DR PROSITE; PS00290; Ig-MHC; 3.						
					KW Immunoglobulin domain; Immunoglobulin C region.						
					FT FT NOLTER; 1						
					FT CONFLICT						
					168 168 R -> N (IN REF. 2).						

FT	CONFLICT	308	P -> L (IN REF. 2).
SEQUENCE	429 AA;	48671 MW;	D2970B34EF8A72B0 CRC64;
Query Match			
Best Local Similarity	77.2%	Score 105; DB 1;	Length 429;
Matches	79 2%	Pred. No. 7.5e-08;	
19; Conservative	1;	Mismatches 4;	Indels 0;
		Gaps 0;	
QY	1	CRVTHPHLPDKTISRISAKPGKRA 24	
Db	289	CRYVHPHPKPVRSITKRGGRS 312	
RESULT 2			
EPC_HUMAN	STANDARD;	PRT;	428 AA.
ID	EPC_HUMAN		
AC	P01854;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DE	16-OCT-2001 (Rel. 40, Last annotation update)		
IGE	epsilon chain C region.		
GN			
OS	Homo sapiens (Human).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=83168897; PubMed=6100763;		
RA	Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,		
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.;		
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon chain cDNA."		
RL	Nucleic Acids Res. 11:719-726(1983).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MAX E.E., Battye J., Ney R., Kirch I.R., Leder P.;		
RA	Cell 29:691-699(1982).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84236029; PubMed=6234164;		
RA	Flanagan J.G., Rabbits T.H.;		
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant region gene, and evidence for three non-allelic genes.";		
EMBO J. 1:655-660(1982).			
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84207910; PubMed=6327276;		
RA	Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;		
RT	"Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudogene that lacks introns.";		
RL	EMBO J. 1:1539-1544(1982).		
RN	[5]		
RP	PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).		
RA	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;		
RL	(TN) Bach M.K. (eds.);		
RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36,		
RL	Marcel Dekker, New York (1978).		
RN	[6]		
RP	SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.		
RX	MEDLINE=83062334; PubMed=6815656;		
RA	Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., Bell L.O., Gould H.J.;		
RT	"Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line.";		
RT	A model of the Fc _α of immunoglobulin E.;"		
RA	Submitted (JUL-1993) to the PDB data bank.		
RESULT 3			
EPC_MOUSE	STANDARD;	PRT;	421 AA.
ID	EPC_MOUSE		
AC	P01856;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	epsilon chain C region.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84236092; PubMed=6329728;		
RA	Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;		
RT	"The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison with the human epsilon gene sequence.";		
EMBO J. 1:1117-1123(1982).			
RN	[2]		
RP	REVSTONS		

DR InterPro: IPR000048; IQ.
 DR InterPro: IPR004009; Myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR001609; myosin_head.
 DR Pfam: PF00612; IQ; 2.
 DR Pfam: PF00033; myosin_head; 1.
 DR Pfam: PF02736; Myosin_N; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PRO0193; MYOSINHEAVY.
 DR PRODOM: PDO00355; myosin_head; 1.
 DR SMART: SM00115; IQ; 1.
 DR PROSITE: PS5006; IQ; 1.
 KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
 KW ATP-binding; Methylation; Alkylation; Multigene family;
 KW Calmodulin-binding.
 FT DOMAIN 1 781 MYOSIN HEAD-LIKE.
 FT DOMAIN 782 811 IQ.
 FT DOMAIN 842 1938 COILED COIL (POTENTIAL).
 FT DOMAIN 177 184 NIP.
 FT DOMAIN 656 678 ACTIN-BINDING.
 FT DOMAIN 758 772 ACTIN-BINDING.
 FT DOMAIN 769 806 CALMODULIN BINDING (BY SIMILARITY).
 FT DOMAIN 815 832 CALMODULIN BINDING (BY SIMILARITY).
 FT MOD_RES 128 128 METHYLATION (TRI-) (POTENTIAL).
 FT MOD_RES 696 696 ALKYLATION (SH-1) (POTENTIAL).
 FT CONFLICT 705 705 ALKYLATION (SH-2) (POTENTIAL).
 FT CONFLICT 13 13 R -> AP (IN REF. 3).
 FT CONFLICT 46 52 V -> A (IN REF. 3).
 FT CONFLICT 51 52 VS -> AP (IN REF. 3).
 FT CONFLICT 87 87 E -> Q (IN REF. 3).
 FT CONFLICT 109 109 MISSING (IN REF. 3).
 FT CONFLICT 1566 1566 F -> FF (IN REF. 4).
 FT CONFLICT 1575 1575 R -> S (IN REF. 4).
 FT CONFLICT 1721 1721 N -> T (IN REF. 4).
 FT CONFLICT 1852 1852 T -> D (IN REF. 4).
 FT CONFLICT 1870 1870 D -> N (IN REF. 4).
 FT CONFLICT 1934 1934 M -> I (IN REF. 4 AND 5).
 SQ SEQUENCE 1938 AA; 223507 MW: D7BD3JFCB19E3C2 CRC64;

Query Match 39.7% Score 54; DB 1; Length 1938;
 Best Local Similarity 50.0%; Conservative 50.0%; Mismatches 3; Indels 7; Gaps 0; Gaps 0;

Qy 2 RVTHPLPKDIVRSIAKPG 21
 Db 664 RTHPHFVRCIIPNERKAPG 683

RESULT 5
 MYH6_HUMAN STANDARD; PRT: 1939 AA.
 AC P13533; Q13943; Q14906; Q14907; PRT: 1939 AA.
 DT 01-JAN-1990 (rel. 13, Created).
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DE 16-OCT-2001 (rel. 40, Last annotation update)
 GN Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=>2131665; PubMed=1776652;
 RA Matsushita R., Beisel K.W., Furukawa M., Arai S., Takao A.;
 RT "Complete sequence of human cardiac alpha-myosin heavy chain gene and
 RT amino acid comparison to other myosins based on structural and
 RT functional differences";
 An. J. Med. Genet. 41:537-547(1991).
 RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE=9410346; PubMed=8307559;
 RA Epp T.A., Dixon I.M., Wang H.Y., Sole M.J., Liew C.-C.;
 RT "Structural organization of the human cardiac alpha-myosin heavy
 RT chain gene (NM_6).";
 RL Genomics 18:505-509(1993).
 RN [3]
 RP SEQUENCE OF 1-177 AND 1551-1939 FROM N.A.
 RX MEDLINE=8926445; PubMed=2726733;
 RA Yamada-Takahara K., Sole M.J., Liew J., Ing D., Liew C.-C.;
 RT "Characterization of human cardiac myosin heavy chain genes. I;
 proc. Natl. Acad. Sci. U.S.A. 86:3504-3508(1989).
 RL [4]
 RP ERRATUM.
 RA Yamada-Takahara K., Sole M.J., Liew J., Ing D., Liew C.-C.;
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7416-7417(1989).
 RN [5]
 RP SEQUENCE OF 1407-1939 FROM N.A.
 RX MEDLINE=88299163; PubMed=2969919;
 RA Kurabayashi M., Tsuchimochi H., Komuro I., Takaku F., Yazaki Y.;
 RT "Molecular cloning and characterization of human cardiac alpha- and
 beta-form myosin heavy chain complementary DNA clones. Regulation of
 RT expression during development and pressure overload in human
 atrium";
 RL J. Clin. Invest. 82:524-531(1988).
 CC -- FUNCTION: MUSCLE CONTRACTION.
 CC -- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC -- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
 CC -- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -- PBM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
 CC -- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUBFRAGMENT (S2).
 CC -- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -- SIMILARITY: CONTAINS 1 IQ DOMAIN.
 CC -- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC
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DR EMBL: D00943; BAA00791; 1;
 DR EMBL: 220566; CA9675; 1;
 DR EMBL: M25110; AAA60386; 1;
 DR EMBL: M25162; AAA0386; 1; JOINED.
 DR EMBL: M25142; AAA0387; 1;
 DR EMBL: M25141; AAA0387; 1; JOINED.
 DR EMBL: M21664; AAA6344; 1;
 DR PIR: A46762; A46764;
 DR PIR: A28908; A28908;
 DR HSSP: P08799; 1; IMMEDIATE.
 DR MIN; 160710;
 DR InterPro; IPR000048; IQ.
 DR InterPro; IPR004009; Myosin_N.
 DR InterPro; IPR002928; Myosin_tail.
 DR InterPro; IPR001609; myosin_head.
 DR PIR: PE00612; IQ; 2;
 DR Pfam: PF00063; myosin_head; 1.
 DR Pfam: PF02736; Myosin_N; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PRO0193; MYOSINHEAVY.
 DR PRODOM: PDO00355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.

DR	SMART; SM00242; MSc; 1.	RX	MEDLINE=86205859; PubMed=3458174;
DR	PROSITE; PS0056; IQ; 1.	RA	Lew C.-C.; Jandreski M.A.;
KW	Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;	RT	"Construction and characterization of the alpha form of a cardiac
KW	ATP-binding; Methylation; Alkylation; Multigene family;	RT	myosin heavy chain cDNA clone and its developmental expression in the
KW	Calmodulin-binding.	RT	Syrian hamster".
FT	DOMAIN 1 782	RL	Proc. Natl. Acad. Sci. U.S.A. 83:3175-3179(1986).
FT	DOMAIN 783 812	CC	-1- FUNCTION: MUSCLE CONTRACTION.
FT	DOMAIN 842 1939	CC	-1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
FT	NP-BIND 178 185	CC	HEAVY CHAIN SUBUNITS (MHC), 2 RAIL LIGHT CHAIN SUBUNITS (MLC)
FT	DOMAIN 657 679	CC	AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
FT	DOMAIN 759 773	CC	-1- DOMAIN: THE ROD-LIKE TATI SEQUENCE IS HIGHLY REPETITIVE, SHOWING
FT	MOD-RES 129 129	CC	CYCLES OF A 26 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
FT	MOD-RES 697 697	CC	-1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
FT	MOD-RES 707 707	CC	ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPase ACTIVITY (BY
FT	CONFICT 88 88	CC	SIMILARITY).
FT	CONFICT 574 574	CC	-1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
FT	CONFICT 608 708	CC	MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
FT	CONFICT 744 744	CC	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
FT	CONFICT 790 790	CC	SUBFRAGMENT (S2).
FT	CONFICT 1014 1014	CC	-1- MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE
FT	CONFICT 1021 1021	CC	MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
FT	CONFICT 1101 1101	CC	-1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
FT	CONFICT 1290 1290	CC	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
FT	CONFICT 1373 1373	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
FT	CONFICT 1533 1533	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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FT	CONFICT 1705 1705	CC	modified and this statement is not removed. Usage by and for commercial
FT	CONFICT 1733 1733	CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
FT	CONFICT 1734 1734	CC	or send an email to license@isb-sib.ch).
FT	CONFICT 1737 1737	CC	-----
FT	CONFICT 1763 1763	CC	DR
FT	CONFICT 1788 1788	CC	InterPro: IPR00048; IQ.
FT	CONFICT 1871 1871	CC	DR
FT	CONFICT 1882 1882	CC	InterPro: IPR00403; Myosin_N.
FT	CONFICT 1890 1890	CC	DR
FT	CONFICT 1933 1933	CC	InterPro: IPR002928; Myosin_tail.
FT	SEQUENCE 1939 AA; 223689 MN; EBCB8/E7CE8768B6F CRC64;	DR	InterPro: IPR002928; Myosin_head.
Query Match	39.7%; Score 54; DB 1; Length 1939;	DR	DR
Best Local Similarity	50.0%; Pred. No. 8;	DR	Pfam: PF00635; myosin_head; 1.
Matches	10; Conservative	DR	Pfam: PF02176; Myosin_N; 1.
OY	2 RYTHPHLPKDIVNSIAKPG 21	DR	Pfam: PF00512; IQ; 2.
Db	665 RYTHPHFVRCIIRERKAPG 684	DR	Pfam: PF00512; IQ; 2.
RESULT	6	DR	PRINS; PR00193; MYOSINHEAVY.
ID	NYH6_MECAU	DR	PRODOM; PD00035; myosin_head; 1.
ID	NYH6_MECAU STANDARD;	DR	SMART; SM00015; IQ; 1.
AC	P13539; Q60562;	DR	SMART; SM00242; MSc; 1.
DT	01-JAN-1990 (rel. 13, 'Created')	DR	PROSITE; P50096; IQ; 1.
DT	15-DEC-1998 (rel. 37, 'Last sequence update')	DR	PROSITE; P50096; IQ; 1.
DT	16-OCT-2001 (rel. 40, 'Last annotation update')	DR	PROSITE; P50096; IQ; 1.
DE	Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha).	DR	PROSITE; P50096; IQ; 1.
GN		DR	PROSITE; P50096; IQ; 1.
OS	Mesocricetus auratus (Golden hamster).	DR	PROSITE; P50096; IQ; 1.
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;	DR	PROSITE; P50096; IQ; 1.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;	DR	PROSITE; P50096; IQ; 1.
OC	Mesocricetus auratus (Golden hamster).	DR	PROSITE; P50096; IQ; 1.
OX	NCBI_TAXID=10036;	DR	PROSITE; P50096; IQ; 1.
RN	[1]	DR	Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
RN	SEQUENCE FROM N.A.	DR	KW
RC	STRAIN=F1B; TISSUE=Liver.	DR	ATP-binding; Methylation; Alkylation; Multigene family;
RX	MEDLINE=95115033; Published=7815459;	DR	Calmodulin-binding.
RA	Wang R., Sole M.J., Cukerman E., Liev C.-C.;	FT	DOMAIN 1 782
RA	"Characterization and nucleotide sequence of the cardiac alpha-myosin	FT	DOMAIN 783 812
RT	heavy chain gene from Syrian hamster.", J. Mol. Cell. Cardiol. 26:1155-1165(1994).	FT	MOD-RES 1439 1443
RT	J. Mol. Cell. Cardiol. 26:1155-1165(1994).	FT	NP-BIND 178 185
RN	[2]	FT	ACTIN-BINDING.
RP	SEQUENCE OF 1630-1939 FROM N.A.	FT	CONFICT 1693 1693
RP		FT	CONFICT 1844 1844
RP		FT	CONFICT 1879 1879
RP		FT	CONFICT 1885 1885
RP		FT	CONFICT 1907 1907
RP		FT	CONFICT 1928 1928
RP		FT	CONFICT 1933 1935
RP		FT	CONFICT 1935 1935

SQ	SEQUENCE	1939 AA;	23626 MW;	DBC8297DFE83115A CRC64;	DR	HSSP; P08799; 1MAD.
Query Match		39.7%	Score 54;	DB 1;	DR	SWISS-2DPAGE; 002566; MOUSE.
Best Local Similarity		50.0%	Pred. No. 8.7;	DR	MGI; MGI:07255; Myhc.	
Matches	10;	Conservative	3;	DR	InterPro; IPR000048; IQ.	
Qy	2	RVTIPHPLPKDIVSIKAPG 21		DR	InterPro; IPR004099; Myosin_N.	
Db	665	RVTIPHPLPKDIVSIKAPG 684		DR	InterPro; IPR00298; Myosin_tail.	
RESULT	7			DR	InterPro; IPR001609; myosin_head.	
MYH6_MOUSE		STANDARD;	PRT;	DR	Pfam; PF0063; myosin_head; 1.	
ID	MYH6_MOUSE			DR	Pfam; PF02736; Myosin_N; 1.	
AC	Q02566; Q64228; 064228; 064788;			DR	Pfam; PF01576; Myosin_tail; 1.	
DT	15-JUL-1998	(Rel. 36; Created)		DR	PRINTS; PRO0193; MYOSINHEAVY.	
DT	16-OCT-2001	(Rel. 40; Last annotation update)		DR	SMART; SM00242; MYSC; 1.	
DE	Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha).			DR	PROSITE; PS50096; IQ; 1.	
GN	MYH6 OR MYHA			DR	PRODOM; PDO0015; IQ; 1.	
OS	MUS musculus (Mouse)			DR	PRINTS; PRO0015; MYOSINHEAVY.	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			DR	SMART; SM00015; IQ; 1.	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			DR	PRINTS; PRO0015; MYOSINHEAVY.	
OX	NCBI_TaxID=10090;			DR	PROSITE; PS50096; IQ; 1.	
RN	[1]			DR	PRINTS; PRO0015; MYOSINHEAVY.	
RP	SEQUENCE FROM N.A.			DR	SMART; SM00015; IQ; 1.	
RC	STRAIN=BALB/C; A/J; C57BL/6J; AND DBA/2J;			DR	PRINTS; PRO0015; MYOSINHEAVY.	
RX	MEDLINE=92250040; PubMed=157481;			DR	SMART; SM00015; IQ; 1.	
RA	Quinn-Laquer B.K., Kennedy J.E., Wel S.J., Peisach K.W.;			DR	PRINTS; PRO0015; MYOSINHEAVY.	
RT	"Characterization of the allelic differences in the mouse cardiac			DR	SMART; SM00015; IQ; 1.	
RT	alpha-myosin heavy chain coding sequence.";			DR	PRINTS; PRO0015; MYOSINHEAVY.	
RL	Genomics 13:176-188(1992).			DR	SMART; SM00015; IQ; 1.	
RN	[2]			DR	PRINTS; PRO0015; MYOSINHEAVY.	
RP	SEQUENCE OF 1-67 FROM N.A.			DR	SMART; SM00015; IQ; 1.	
RC	STRAIN=AKR;			DR	PRINTS; PRO0015; MYOSINHEAVY.	
RX	MEDLINE=9125025; PubMed=2026617;			DR	SMART; SM00015; IQ; 1.	
RA	Gulick J., Subramanian A., Neumann J., Robbins J.,			DR	PRINTS; PRO0015; MYOSINHEAVY.	
RT	"Isolation and characterization of the mouse cardiac myosin heavy			DR	SMART; SM00015; IQ; 1.	
RT	chain genes.";			DR	PRINTS; PRO0015; MYOSINHEAVY.	
RL	J. Biol. Chem. 266:9180-9185(1991).			DR	SMART; SM00015; IQ; 1.	
CC	- - SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)			DR	PRINTS; PRO0015; MYOSINHEAVY.	
CC	CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).			DR	SMART; SM00015; IQ; 1.	
CC	- - SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.			DR	PRINTS; PRO0015; MYOSINHEAVY.	
CC	- - DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPATAPPTIDES,			DR	SMART; SM00015; IQ; 1.	
CC	CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.			DR	PRINTS; PRO0015; MYOSINHEAVY.	
CC	- - DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPATAPPTIDES,			DR	SMART; SM00015; IQ; 1.	
CC	CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.			DR	PRINTS; PRO0015; MYOSINHEAVY.	
CC	- - PTM: TWO CYSTINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.			DR	PRINTS; PRO0015; MYOSINHEAVY.	
CC	- - MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMOTIN (LMN) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).			DR	PRINTS; PRO0015; MYOSINHEAVY.	
CC	- - MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.			DR	PRINTS; PRO0015; MYOSINHEAVY.	
CC	- - MISCELLANEOUS: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.			DR	PRINTS; PRO0015; MYOSINHEAVY.	
CC	- - SIMILARITY: CONTAINS 1 IQ DOMAIN.			DR	PRINTS; PRO0015; MYOSINHEAVY.	
CC	CC	CC	CC	CC	CC	CC
CC	THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION - THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL ENTITIES REQUIRES A LICENSE AGREEMENT (SEE HTTP://WWW.EBI.SIB-SIB.CH/ANNOUNCE/ OR SEND AN EMAIL TO LICENSE@EBI.SIB.CH).					
CC						
DR	M76598; AAA37159; 1;			DR	SEQUENCE FROM N.A.	
DR	EMBL; M76599; AAA37160; 1;			DR	SEQUENCE OF 774-1940 FROM N.A.	
DR	EMBL; M76500; AAA37161; 1;			DR	SEQUENCE OF 903-3298; PubMed=280546;	
DR	EMBL; M76501; AAA37162; 1;			DR	MEDLINE=9033298; PubMed=280546;	
DR	EMBL; M62404; AAA37424; 1;			DR	ELIER M.S., STEEDMAN H.H., SYVETER J.E., FERTELS S.H., WU Q.-L., RAYCHOWDHURY M.K., RUBINSTEIN M.A., KELLY A.M., SARVAR S.; Human embryonic myosin heavy chain cDNA. Interspecies sequence	

Mon Jul 15 13:22:30 2002

RT	conservation of the myosin rod, chromosomal locus and isoform	FT	NP-BIND	179	186	ATP (POTENTIAL).	
RT	specific transcription of the gene.";	FT	DOMAIN	656	678	ACTIN-BINDING.	
FERS Lett.	256:21-28(1989),	FT	DOMAIN	758	772	ACTIN-BINDING.	
RL	[3]	FT	DOMAIN	130	130	METHYLATION ("TRI-") (POTENTIAL).	
RN	SEQUENCE OF 855-1940 FROM N.A.	FT	MOD-RES	696	696	ALKYLATION (SH-2).	
RP	TISSUE-Skeletal muscle;	FT	MOD-RES	706	706	ALKYLATION (SH-3).	
RC	Medline=9023582; PubMed=1691080;	FT	CONFICT	1331	1331	A -> G (IN REF. 3).	
RX	Medline=9023582; PubMed=1691080;	FT	CONFICT	1391	1392	KK -> QE (IN REF. 1 AND 2).	
RA	Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,	FT	CONFICT	1608	1609	SR -> RA (IN REF. 3).	
RA	Arnold H.H.;	FT	CONFICT	1663	1664	RG -> QT (IN REF. 2).	
RT	"Identification of three developmentally controlled isoforms of human	FT	SEQUENCE	1940	AA:	CRC64;	
RT	myosin heavy chains";	DB	664	RTHPHFVRCITPNETKTPG	683	43CA5BC6A4BA1253	
RN	Bur. J. Biochem. 189:55-65(1990).	Query Match	37.5%	Score	51;	DB 1;	
RN	[4]	Best Local Similarity	45.0%	Pred. No.	24;	Length 1940;	
RP	SEQUENCE OF 856-1940 FROM N.A.	Matches	9;	Mismatches	3;	Gaps 0;	
RA	Medline=93366648; PubMed=2771643;	Oy	2	RVTPHPLRDIYRSIAKAVP	21		
RX	Karsch-Mirachini I., Travis M., Blau H., Reinward L.A.;	ID	MYH3-RAT				
CC	"Expression and DNA sequence analysis of a human embryonic skeletal	AC	MYH3-RAT				
CC	muscle myosin heavy chain gene";	DT	P12847;				
CC	Nucleic Acids Res. 17:6167-6179(1989).	DT	01-OCT-1989 (Rel. 12, Created)				
CC	NUCLEIC ACIDS RES.	DT	01-OCT-1989 (Rel. 12, Last sequence update)				
CC	-1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2	DT	16-OCT-2001 (Rel. 40, Last annotation update)				
CC	HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)	DE	Myosin heavy chain, fast skeletal muscle, embryonic.				
CC	AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).	GN	GN				
CC	-1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.	OS	Rattus norvegicus (Rat);				
CC	AND DEVELOPMENTAL STAGE: ABUNDANTLY PRESENT IN FETAL SKELETAL	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	AND NOT PRESENT OR BARELY DETECTABLE IN HEART AND ADULT SKELETAL	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
CC	MUSCLE.	OX	NCBI_TaxID:16116;				
CC	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING	RA	[1]				
CC	CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,	RP	SEQUENCE FROM N.A.				
CC	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED	RA	Strehler E.E., Strehler-Page M.A., Perrard J.C., Periasamy M.,				
CC	SUBFRAGMENT (S2). 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.	RA	Nadal-Ginard B.,				
CC	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.	RA	"Complete nucleotide and encoded amino acid sequence of a mammalian				
CC	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.	RT	myosin heavy chain gene. Evidence against intron-dependent evolution				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	RT	of the rod.";				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	RT	J. Mol. Biol. 190:291-317(1986).				
CC	the European Bioinformatics Institute. There are no restrictions on its	RL	-1- FUNCTION: MUSCLE CONTRACTION.				
CC	use by non-profit institutions as long as its content is in no way	CC	-1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2				
CC	modified and this statement is not removed. Usage by and for commercial/	CC	HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)				
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch.)	CC	AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).				
CC	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING	CC	-1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.				
CC	CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,	CC	-1- FUNCTION: MUSCLE CONTRACTION.				
CC	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED	CC	-1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2				
CC	SUBFRAGMENT (S2). 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.	CC	HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)				
CC	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.	CC	AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).				
CC	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.	CC	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	CC	CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	CC	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED				
CC	the European Bioinformatics Institute. There are no restrictions on its	CC	SUBFRAGMENT (S2). 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.				
CC	use by non-profit institutions as long as its content is in no way	CC	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
CC	modified and this statement is not removed. Usage by and for commercial/	CC	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch.)	CC	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
DR	EMBL; X13988; CA32167.1; -;	CC	DR	NP-BIND	179	186	ATP (POTENTIAL).
DR	EMBL; X15193; CA35942.1; -;	CC	DR	DOMAIN	656	678	ACTIN-BINDING.
DR	EMBL; X15196; CA33731.1; -;	CC	DR	DOMAIN	758	772	ACTIN-BINDING.
DR	EMBL; X15196; S04090.	CC	DR	MOD-RES	130	130	METHYLATION ("TRI-") (POTENTIAL).
DR	PIR; P08759; IMM.	CC	DR	MOD-RES	696	696	ALKYLATION (SH-2).
DR	HSSP; P08759; IMM.	CC	DR	MOD-RES	706	706	ALKYLATION (SH-3).
DR	MIM: 160720; -;	CC	DR	CONFICT	1331	1331	A -> G (IN REF. 3).
DR	EMBL; X13100; CA31492.1; -;	CC	DR	CONFICT	1391	1392	KK -> QE (IN REF. 1 AND 2).
DR	EMBL; X15193; CA35942.1; -;	CC	DR	CONFICT	1608	1609	SR -> RA (IN REF. 3).
DR	EMBL; X15196; S04090.	CC	DR	CONFICT	1663	1664	RG -> QT (IN REF. 2).
DR	PIR; P08759; IMM.	CC	DR	SEQUENCE	1940	AA:	CRC64;
DR	MIM: 160720; -;	CC	DR	664	RTHPHFVRCITPNETKTPG	683	43CA5BC6A4BA1253
DR	INTERPRO: IPR000048; IO: 1.	Query Match	37.5%	Score	51;	DB 1;	
DR	INTERPRO: IPR000009; Myosin_N.	Best Local Similarity	45.0%	Pred. No.	24;	Length 1940;	
DR	INTERPRO: IPR00028; Myosin_tail.	Matches	9;	Mismatches	3;	Gaps 0;	
DR	INTERPRO: IPR001609; myosin_head.	Oy	2	RVTPHPLRDIYRSIAKAVP	21		
DR	Pfam: PF00512; IO: 2.	ID	MYH3-RAT				
DR	Pfam: PF00083; myosin_head; 1.	AC	MYH3-RAT				
DR	Pfam: PF02736; Myosin_N; 1.	DT	P12847;				
DR	Pfam: PF01576; Myosin_tail; 1.	DT	01-OCT-1989 (Rel. 12, Created)				
DR	PRINTS; PRO0193; MYOSINHEAVY.	DT	01-OCT-1989 (Rel. 12, Last sequence update)				
DR	PRODOM; PD00035; myosin_head; 1.	DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DR	SMART; SM0015; IQ: 1.	DE	Myosin heavy chain, fast skeletal muscle, embryonic.				
DR	SMART; SM00242; MSC; 1.	GN	GN				
DR	PROSITE; PS50096; IO: 1.	OS	Rattus norvegicus (Rat);				
DR	PROSITE; PS50096; IO: 1.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
DR	PROSITE; PS50096; IO: 1.	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
DR	EMBL; X13988; CA32167.1; -;	OX	NCBI_TaxID:16116;				
FT	Multitene family.	RA	[1]				
FT	1. MYOSIN HEAD-LIKE.	RP	SEQUENCE FROM N.A.				
FT	781 IQ.	RA	Strehler E.E., Strehler-Page M.A., Perrard J.C., Periasamy M.,				
FT	811 IQ.	RA	Nadal-Ginard B.,				
FT	COILED COIL (POTENTIAL).	RA	"Complete nucleotide and encoded amino acid sequence of a mammalian				
FT	840 1933	RA	myosin heavy chain gene. Evidence against intron-dependent evolution				
FT	DOMAIN	RA	of the rod.";				
FT	DOMAIN	RA	J. Mol. Biol. 190:291-317(1986).				
FT	DOMAIN	RA	-1- FUNCTION: MUSCLE CONTRACTION.				
FT	DOMAIN	RA	-1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2				
FT	DOMAIN	RA	HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)				
FT	DOMAIN	RA	AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).				
FT	DOMAIN	RA	-1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.				
FT	DOMAIN	RA	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING				
FT	DOMAIN	RA	CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,				
FT	DOMAIN	RA	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED				
FT	DOMAIN	RA	SUBFRAGMENT (S2). 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.				
FT	DOMAIN	RA	CHARACTERISTIC RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY				
FT	DOMAIN	RA	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING				
FT	DOMAIN	RA	CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,				
FT	DOMAIN	RA	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED				
FT	DOMAIN	RA	SUBFRAGMENT (S2). 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	This SWISS-PROT entry is copyright. It is produced through a collaboration				
FT	DOMAIN	RA	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
FT	DOMAIN	RA	the European Bioinformatics Institute. There are no restrictions on its				
FT	DOMAIN	RA	use by non-profit institutions as long as its content is in no way				
FT	DOMAIN	RA	modified and this statement is not removed. Usage by and for commercial/				
FT	DOMAIN	RA	entities requires a license agreement (see http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch.)				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.				
FT	DOMAIN	RA	CHARACTERISTIC RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY				
FT	DOMAIN	RA	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING				
FT	DOMAIN	RA	CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,				
FT	DOMAIN	RA	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED				
FT	DOMAIN	RA	SUBFRAGMENT (S2). 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	This SWISS-PROT entry is copyright. It is produced through a collaboration				
FT	DOMAIN	RA	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
FT	DOMAIN	RA	the European Bioinformatics Institute. There are no restrictions on its				
FT	DOMAIN	RA	use by non-profit institutions as long as its content is in no way				
FT	DOMAIN	RA	modified and this statement is not removed. Usage by and for commercial/				
FT	DOMAIN	RA	entities requires a license agreement (see http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch.)				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.				
FT	DOMAIN	RA	CHARACTERISTIC RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY				
FT	DOMAIN	RA	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING				
FT	DOMAIN	RA	CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,				
FT	DOMAIN	RA	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED				
FT	DOMAIN	RA	SUBFRAGMENT (S2). 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.				
FT	DOMAIN	RA	CHARACTERISTIC RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY				
FT	DOMAIN	RA	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING				
FT	DOMAIN	RA	CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,				
FT	DOMAIN	RA	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED				
FT	DOMAIN	RA	SUBFRAGMENT (S2). 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.				
FT	DOMAIN	RA	CHARACTERISTIC RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY				
FT	DOMAIN	RA	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING				
FT	DOMAIN	RA	CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,				
FT	DOMAIN	RA	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED				
FT	DOMAIN	RA	SUBFRAGMENT (S2). 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.				
FT	DOMAIN	RA	CHARACTERISTIC RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY				
FT	DOMAIN	RA	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING				
FT	DOMAIN	RA	CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,				
FT	DOMAIN	RA	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED				
FT	DOMAIN	RA	SUBFRAGMENT (S2). 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.				
FT	DOMAIN	RA	CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.				
FT	DOMAIN	RA					

DR InterPro: IPR004009; Myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR003017; Spectrin.
 DR InterPro: IPR001609; myosin_head.
 DR Pfam: PF00053; IQ; 2.
 DR Pfam: PF02136; Myosin_head; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PRO0193; MYSINHEAVY.
 DR PRODOM: PD00035; myosin_head; 1.
 DR SMART: SM0015; IQ; 1.
 DR SMART; SM00242; MUSC; 1.
 KW PROSITE: PS00096; IQ; 1.
 KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation; Multideme family.
 FT DOMAIN 1 781 MYOSIN HEAD-LINE.
 FT DOMAIN 782 811 IQ.
 FT DOMAIN 840 1933 COTLED COIL (POTENTIAL).
 FT NE_BIND 179 186 ATP (POTENTIAL).
 FT DOMAIN 656 678 ACTIN-BINDING.
 FT DOMAIN 758 772 ACTIN-BINDING.
 FT MOD_RES 130 130 METHYLATION (TRI-) (POTENTIAL).
 FT MOD_RES 696 696 ALKYLATION (SH-1).
 FT SEQUENCE 705 706 ALKYLATION (SH-2).
 SQ 1940 AA: 223857 MW: 85D546A596E5A696 CRC64;

Query Match
 Best Local Similarity 37.5%; Score 51; DB 1; Length 1940;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 RYTHPHLPDKIVRSIAKPG 21
 Db 664 RYTHPHFVRCIIPNETKPG 683

RESULT 10

ID	GC4_HUMAN	STANDARD:	PRT:	327 AA.
AC	PO1861;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DE	16-Oct-2001 (Rel. 40, Last annotation update)			
GN	IGHG4			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:83157104; PubMed=6299662;			
RA	Ellison J.W., Buxbaum J.N., Hood L.E.;			
RT	"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";			
RL	DNA 1:1-18(1981).			
RN	[2]			
RP	SEQUENCE OF 1-30 AND 81-326.			
RX	MEDLINE=70207560; PubMed=1192699;			
RA	Pink J.R., Buttery S.H., de Vries G.M., Milstein C.;			
RT	"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of gamma 4 chain.";			
RL	Bloch, J. 117:33-47(1970).			
CC	[3]			
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CC	EMBL; K01316; AAC59394.1; ALT_INIT.			

DR PIR: A02150; G4HU.
 DR HSSP: P018842; 7FBAB.
 DR MM: 147130; -.
 DR InterPro: IPR03006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00410; Ig-like; 1.
 DR SMART; SM00215; IQ; 1.
 DR PROSITE: PS00280; Ig_MHC; 2.
 DR Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 98 CH1.
 FT DOMAIN 1 99 110 HINGE.
 FT DOMAIN 111 220 CH2.
 FT DOMAIN 221 327 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 DISULFID 141 201 DISULFID 247 305 DISULFID 327 AA: 35940 MW: 3EDBD81BF208E7A CRC64;

Query Match
 Best Local Similarity 37.1%; Score 50.5; DB 1; Length 327;
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 1 CRYTHPHLPDKIVRSIAKPGK-RAP 25
 Db 201 CKVSNKGLPSSIEKTISKAKGOPREP 226

RESULT 11

ID	GC4A_MOUSE	STANDARD:	PRT:	330 AA.
AC	PO1863;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	30-MAY-2000 (Rel. 01, Last annotation update)			
DE	Ig gamma-2A chain C region, A allele.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OX	NCBI_TaxID=10909;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=107654; PubMed=677755;			
RA	Sikorav J.-L., Auffray C., Rouzeon F.;			
RT	"Structure of the constant and 3 untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA.";			
RT	Balb/c gamma 2a heavy chain messenger RNA.";			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81198976; PubMed=6262729;			
RA	Yamawaki-Katakoma Y., Miyata T., Ronjo T.;			
RT	"The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";			
RT	Nucleic Acids Res. 9:1365-1381(1981).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81122394; PubMed=6787604;			
RA	Ollio R., Auffray C., Morchamps C., Rouzeon F.;			
RT	"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic family.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).			
RL	[4]			
RN	MELOMA PROTEIN MOPC 173			
RP	MEDLINE=417517; PubMed=4831970;			
RA	Bourgois A., Fougerousse M., Rocca-Serra J.			

DR PRODOM; PDB00355; myosin_head; 1.
 DR SMART; SN00015; IQ; 1.
 DR PROSITE; PS0095; TO; 1.
 KW Myosin; Muscle protein; Coiled coil; Thick filament; Alkylation; ATP-binding; Methylation; Multigene family;
 KW Calmodulin-binding; Calmodulin-binding; 1.
 FT DOMAIN 779
 FT DOMAIN 780 809
 FT DOMAIN 839 1934
 FT DOMAIN 177 184
 FT DOMAIN 654 676
 FT DOMAIN 756 770
 FT MOD_RES 128 128
 FT MOD_RES 694 694
 FT MOD_RES 704 704
 FT CONFLICT 966 966
 FT CONFLICT 978 978
 FT CONFLICT 986 986
 FT CONFLICT 1008 1014
 FT CONFLICT 1057 1057
 FT CONFLICT 1060 1060
 FT CONFLICT 1095 1095
 FT CONFLICT 1217 1217
 FT CONFLICT 1271 1271
 FT CONFLICT 1327 1327
 FT CONFLICT 1358 1358
 FT CONFLICT 1504 1504
 FT CONFLICT 1537 1537
 FT CONFLICT 1556 1556
 SQ AA: 222928 MW: FDBAC58310BDB57D CRC564;

Query Match 36.8%; Score 50; DB 1; Length 1934;
 Best Local Similarity 45.0%; Pred. No. 33; 9; Conservative
 Matches 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 RYVHPLPKDVRAKAPG 21
 | ||| | : | : | : |:
 Db 662 RSTPHPRVRCIPNETKSPG 681

RESULT 15

MYH7_HUMAN
 ID MYH7_HUMAN STANDARD; PRT: 1935 AA.
 AC P1283; Q14904; Q16579;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta).
 GN MYH7 OR MYHC-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91065634; PubMed=2249844;
 RA Jaenische T., Diederich K.W., Haas W., Schleicher J., Lichter P.,
 RA Pfleider M., Bach A., Vosberg H.P.;
 RT "The complete sequence of the human beta-myosin heavy chain gene and
 a comparative analysis of its product.";
 RL Genomics 8:194-206(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91031495; PubMed=2362820;
 RA Liew C.-C., Sole M.J., Yamauchi-Takahara K., Kellam B.,
 RA Anderson D.H., Lin L., Liew J.;
 RT "Complete sequence and organization of the human cardiac beta-myosin
 heavy chain gene.";
 RL Nucleic Acids Res. 18:3647-3651(1990).
 RN [3]
 RP SEQUENCE OF 1-115 FROM N.A.

RX MEDLINE=89264452; PubMed=2726733;
 RA Yamadachi-Takahara K., Sole M.J., Liew J., Ing D., Liew C.-C.;
 RA "Characterization of human cardiac myosin heavy chain genes.";
 RT Proc. Natl. Acad. Sci. U.S.A. 86:3504-3508(1989).
 RL [4]
 RN ERATUM.
 RA Yamadachi-Takahara K., Sole M.J., Liew J., Ing D., Liew C.-C.;
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7416-7417(1989).
 RN [5]
 RP SEQUENCE OF 1310-1935 FROM N.A.
 RX MEDLINE=86116778; PubMed=2421254;
 RA Saez L., Leinwand L.A.;
 RT "Characterization of diverse forms of myosin heavy chain expressed in
 adult human skeletal muscle.";
 RL Nucleic Acids Res. 14:2951-2969(1986).
 RN [6]
 RP REVISIONS.
 RA Leinwand L.A.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQENCE OF 1410-1935 FROM N.A.
 RX MEDLINE=88291913; PubMed=2869919;
 RA Kurabayashi M., Tsuichimochi H., Komuro I., Takaku F., Yazaki Y.;
 RT "Molecular cloning and characterization of human cardiac alpha- and
 beta-form myosin heavy chain complementary DNA clones. Regulation of
 expression during development and pressure overload in human
 atrium.";
 RL J. Clin. Invest. 82:524-531(1988).
 RN [8]
 RP SEQUENCE OF 785-1935 FROM N.A.
 RC TISSUE_Skeletal muscle;
 RX MEDLINE=90255865; PubMed=1691980;
 RA Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
 RA Arnold H.H.;
 RT "Identification of three developmentally controlled isoforms of human
 myosin heavy chains";
 RL J. Biol. Chem. 269:189-55-65(1990).
 RN [9]
 RP SEQUENCE OF 1393-1935 FROM N.A.
 RX MEDLINE=87192738; PubMed=3032769;
 RA Janreski M.A., Liow C.-C.;
 RT "Construction of a human ventricular cDNA library and
 characterization of a beta myosin heavy chain cDNA clone.";
 RL Hum. Genet. 76:47-53(1987).
 RN [10]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=96039076; PubMed=8533830;
 RA Arai S., Matsukura R., Hirayama K., Sukurai H., Tamura M., Ozawa T.,
 RA Kimura M., Imaura S.-I., Furutani Y., Joh-O K., Kawana M., Takeo A.,
 RA Hosoda S., Momma K.;
 RT "Missense mutation of the beta-cardiac myosin heavy-chain gene in
 hypertrophic cardiomyopathy";
 RL Am. J. Med. Genet. 58:267-276(1995).
 RN [11]
 RP VARIANTS CMH1_GLIU-256 AND ARG-741.
 RX MEDLINE=93248215; PubMed=8483915;
 RA Fananapazir L., Dalakas M.C., Cyran F., Cohn G., Epstein N.D.,
 RA Geisterer-Lowrance A.R.I., Koss S., Tanigawa G., Vosberg H.-P.,
 RT "Missense mutations in the beta-myosin heavy-chain gene cause central
 core disease in hypertrophic cardiomyopathy";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:3993-3997(1993).
 RN [12]
 RP VARIANTS CMH1_GLU-256 AND ARG-741.
 RX MEDLINE=90367131; PubMed=1795517;
 RA Geisterer-Lowrance A.R.I., Koss S., Tanigawa G., Vosberg H.-P.,
 RA McKenna W., Selzman C.E., Seidman J.G.;
 RT "A molecular basis for familial hypertrophic cardiomyopathy: a beta
 cardiac myosin heavy chain gene missense mutation.";
 RL Cell 62:995-1006(1990).
 RN [13]
 RP VARIANTS CMH1_GLN-249; GLN-403; CYS-453 AND MET-606.
 RX MEDLINE=92204193; PubMed=1529212;
 RA Wakkins H., Rosenzweig A., Bwang D.S., Levi T., McKenna W.,
 RA Seidmann C.E., Seidman J.G.;

RT "Characteristics and prognostic implications of myosin missense mutations in familial hypertrophic cardiomyopathy.";
 RT New Engl. J. Med. 326:1108-1114(1992).
 RN [14] RP VARIANT CMHL GLN-403; CYS-453; ARG-584 AND MET-606.
 RX MEDLINE=90070063; PubMed=8250038;
 RA Watkins H., Thierfelder L., Anan R., Jarcho J., Matsumori A.,
 RA McKenna N.D., Seidman J.G., Seidman C.E.;
 RT "Independent origin of identical beta cardiac myosin heavy-chain mutations in hypertrophic cardiomyopathy.";
 RL Am. J. Hum. Genet. 53:1180-1185(1993).
 RN [15] RP VARIANT CMHL GLN-403 AND VAL-908.
 RX MEDLINE=92193810; PubMed=1638703;
 RA Epstein N.D., Cohn G.M., Cyran F., Fananapazir L.;
 RT "Differences in clinical expression of hypertrophic cardiomyopathy associated with two distinct mutations in the beta-myosin heavy chain gene. A 908Leu-->Val mutation and a 403Arg-->Gln mutation.";
 RL Circulation 86:3345-3352(1992).
 RN [16] RP VARIANT CMHL LEU-403 AND TRP-403.
 RX MEDLINE=94075629; PubMed=8250035;
 RA Dausse E., KomaJda M., Ferrier L., Dubourg O., Dufour C., Carrier L.,
 RA Wisniewsky C., Bercovici J., Hengstenberg C., Al-Mahdawi S.;
 RT "Familial hypertrophic cardiomyopathy. Microsatellite haplotyping and identification of a hot spot for mutations in the beta-myosin heavy chain gene.";
 RL J. Clin. Invest. 92:2807-2813(1993).
 RN [17] RP VARIANT CMHL TRP-403.
 RX MEDLINE=94093668; PubMed=8268932;
 RA Moelman J.C., Brink P.A., Cortfield V.A.;
 RT "Identification of a new missense mutation at Arg403, a CpG mutation hotspot, in exon 13 of the beta-myosin heavy chain gene in hypertrophic cardiomyopathy.";
 RL Hum. Mol. Genet. 2:1731-1732(1993).
 RN [18] RP VARIANT CMHL ASN-615.
 RX MEDLINE=93038698; PubMed=1417858;
 RA Nishi H., Kimura A., Harada H., Toshima H., Sasazuki T.;
 RT "Novel missense mutation in cardiac beta myosin heavy chain gene found in a Japanese patient with hypertrophic cardiomyopathy.";
 RL Biochem. Biophys. Res. Commun. 188:379-387(1992).
 RN [19] RP VARIANT CMHL GLX-778.
 RX MEDLINE=93343938; PubMed=83343162;
 RA Harada H., Kimura A., Nishi H., Sasazuki T., Toshima H.;
 RT "A missense mutation of cardiac beta myosin heavy chain gene linked to familial hypertrophic cardiomyopathy in affected Japanese families.";
 RL Biochem. Biophys. Res. Commun. 194:791-798(1993).
 RN [20] RP VARIANT CMHL VAL-908.
 RX MEDLINE=93168405; PubMed=8435239;
 RA Ali Mandewi S., Chamberlain S., Cleland J., Nihoyannopoulos P., Gilligan D., French J., Choudhury L., Williamson R., Oakley C.;
 RT "Identification of a mutation in the beta cardiac myosin heavy chain gene in a family with hypertrophic cardiomyopathy.";
 RL Br. Heart J. 69:136-141(1993).
 RN [21] RP VARIANT CMHL TRP-719.
 RX MEDLINE=95179132; PubMed=874131;
 RA Greve G., Bachinski L., Friedman D.L., Czernuszewicz G., Anan R., Towbin J., Seidman C.E., Roberts R.;
 RT "Isolation of a de novo mutant myocardial beta MHC protein in a pedigree with hypertrophic cardiomyopathy.";
 RL Hum. Mol. Genet. 3:2073-2075(1994).
 RN [22] RP VARIANT CMHL CYS-513; ARG-716 AND TRP-719.
 RX MEDLINE=94110336; PubMed=828298;
 RA Anan R., Greve G., Thierfelder L., Watkins H., McKenna N., Solomon S., Vecchio C., Shono H., Nakao S., Tanaka H., Mares A. Jr., Towbin J.A., Spirito R., Roberts R., Seidman J.G., Seidman C.E.;

RT "Prognostic implications of novel beta cardiac myosin heavy chain gene mutations that cause familial hypertrophic cardiomyopathy.";
 RT RL J. Clin. Invest. 93:280-285(1994).
 RN [23] RP VARIANT CMHL THR-79.
 RX MEDLINE=96047159; PubMed=7581410;
 RA Moellman J.C., Brink P.A., Cortfield V.A.;
 RT "Identification of a novel Ala79Thr mutation in exon 21 of the beta-myosin heavy chain gene in hypertrophic cardiomyopathy.";
 RL Hum. Mutat. 6:197-198(1995).
 RN [24] RP VARIANT CMHL CYS-453.
 RX MEDLINE=96209901; PubMed=8655135;
 RA Ko Y.-L., Chen J.-J., Tang T.-K., Cheng J.-J., Lin S.-Y., Liou Y.-C.,
 RA Kuan P., Wu C.-W., Lien W.-P., Liew C.-C.;
 RT "Malignant familial hypertrophic cardiomyopathy in a family with a 45Arg-->Cys mutation in the beta-myosin heavy chain gene: coexistence of sudden death and end-stage heart failure.";
 RT RL Hum. Genet. 97:585-590(1996).
 RN [25] RP VARIANT CMHL THR-349 AND TRP-719.
 RX MEDLINE=98204402; PubMed=8541842;
 RA Jeschke B., Uhl K., Weist B., Schroder D., Meitinger T.,
 RA Domke C., Vosberg H.-P.;
 RT "A high risk phenotype of hypertrophic cardiomyopathy associated with Best Local Similarity 36.8%; Score 50; DB 1; Length 1935;
 Query Match 45.0%; Pred. No. 33;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 Db 663 RSTHPHEVRCIIPNETKSPG 682

Search completed: July 15, 2002, 12:49:43
 Job time: 204 sec

Qy	1	CRYTHPHILPKIVRSIAKPGK	22	KW	Hypothetical protein; Complete proteome;
Db	645	CLVGHPSLNRDILRSTNKSNG	666	SEQUENCE	273 AA; 29461 MW; C1C6D2FB7E432082 CRC64;
RESULT	2	PRELIMINARY;	PRT;	OS	Oryctolagus cuniculus (Rabbit)
ID	09MVS5			OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
AC	09MVS5;	`		OC	Mammalia; Eutheria; Lagomorpha; Oryctolagus.
DR	01-OCT-2000	(TREMBLrel. 15'	Created)	OX	NCBI-TaxID=9986;
DT	01-OCT-2000	(TREMBLrel. 15'	Last sequence update)	RN	[1]
DE	01-DEC-2001	(TREMBLrel. 19'	Last annotation update)	RP	SEQUENCE FROM N.A.
DE	MYOSIN HEAVY CHAIN (FRAGMENT).			RC	STRAIN=N.E. STRAIN=NEW ZEALAND WHITE; TISSUE=HEART;
GN	GN			RA	Sayed R.A., Grace A.A., Vandenehegh J.I.;
OS				RA	"Patterns of ion channel expression in cardiac hypertrophy.";
OC				RL	Submitted [JUN-2000] to the EMBL/GenBank/DDBJ databases.
OX				DR	EMBL: AU291317; CABN948491; HSSP: P13358; 2MYS;
RN				DR	InterPro: IPR001609; Pfam: PF0063; myosin_head; PRODOM: PD000355; myosin_head; NON_TER: 1;
RP				FT	SEQUENCE
RC				SQ	99 AA; 10933 MW; 3961CA1047DB2E0C CRC64;
RC					Query Match Best Local Similarity 39.7%; Score 54; DB 6; Length 99; Pred. No. 1.7; Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
RC					Query Match Best Local Similarity 50.0%; Score 54; DB 6; Length 99; Pred. No. 1.7; Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Qy	2	VTHPHLPKIVRSIAKPG	21	OS	Caulobacter crescentus.
Db	79	RITTHPHFVRCILPNERKAPG	98	OS	Bacteria; Proteobacteria; alpha subdivision; Caulobacter group; NCBI_TaxID=69394; [1]
RESULT	3			OS	SEQUENCE FROM N.A.
ID	09AAN3	PRELIMINARY;	PRT;	AC	09AAN3;
AC	09AAN3;			AC	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	HYPOTHETICAL PROTEIN CC0564.			DE	HYPOHETICAL PROTEIN CC0564.
GN	GN			DR	REDENBACH M., KIEFER H.-M., DENAPATRE D., EICHNER A., CULLUM J., KINASHI H., HOPWOOD D.A.; "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
GN	GN			DR	MOL. MICROBIOL. 21:77-96(1995); EMBL: AL05161; CNA22724.1; -.
RP				KW	HYPOTHETICAL PROTEIN.
RP				SQ	SEQUENCE 197 AA; 21061 MW; 6ABC3643C5570AC1 CRC64;
RP					Query Match Best Local Similarity 37.5%; Score 51; DB 2; Length 197; Pred. No. 9.7; Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
RP					Query Match Best Local Similarity 42.9%; Score 51; DB 2; Length 197; Pred. No. 9.7; Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
RC				Qy	3 VTHPHLPKIVRSIAKPG
RC				Qy	3 VTHPHLPKIVRSIAKPG
RC				DR	23 : : : ; 177 LAHPPLAQAVRALAPIGOR 197
RC				RESULT	5
RC				Q989RB	PRELIMINARY;
RC				AC	Q9K9RB;
RC				DR	01-OCT-2000 (TREMBLrel. 15' Created)
RC				DT	01-OCT-2000 (TREMBLrel. 15' Last sequence update)
RC				DT	01-OCT-2000 (TREMBLrel. 15' Last annotation update)
RC				DE	BH2577 PROTEIN.
RC				GN	Bacillus halodurans.
RC				OS	Bacteria; Firmicutes; Bacillus/Clostridium group;
RC				OC	Bacillus/Staphylococcus group; Bacillus.
RC				OX	NCBI-TaxID=86665;
RC				NN	[1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuwara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*."
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001516; BAB0296 1; -.
 KW Complete Proteome.
 SQ SEQUENCE 538 AA; 62270 MW; 470E31DE2FC0C507 CRC64;

Query Match 37.1%; Score 50.5; DB 16; Length 538;
 Best Local Similarity 41.7%; Pred. No. 33; Mismatches 9; Indels 1; Gaps 1;
 Matches 10; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 2 RVTTHPLHP-KDIVRSIKA[P]RKA 24
 :: ||| | | : ||| |
 Db 431 QIRHSHKPIKDLARQIGETPGKLA 454

RESULT 6

Q9UQB8 PRELIMINARY; PRT; 68 AA.

ID Q9UQB8
 AC Q9UQB8;
 DT 01-MAY-2000 (TREMBREL. 13, Created)
 DT 01-MAY-2000 (TREMBREL. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBREL. 19, Last annotation update)

DB BETA-MYOSIN HEAVY CHAIN (FRAGMENT).

OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TAXID=9606;
 RN [1]

RN SEQUENCE FROM N.A.
 RK MEDLINE=0914425; PubMed=2522082;
 RA Diederich K.W., Eisele T., Riedl T., Jaenische T., Lichter P.,
 RA Vosberg H.P.;
 RT "Isolation and characterization of the complete human beta-myosin heavy chain gene.";
 RT Hum. Genet. 81:214-220(1989).
 DR EMBL; M77636; AAA79019.1; -.
 DR HSSP; P13538; 2WS;
 DR InterPro; IPR001609; myosin_head.
 DR Pfam; PF00063; myosin_head; 1.
 DR ProDom; PD000355; myosin_head; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 68 AA; 7890 MW; B58C9D8951B4D1C2 CRC64;

Query Match 36.8%; Score 50; DB 4; Length 68;
 Best Local Similarity 45.0%; Pred. No. 4.5; Mismatches 7; Indels 0; Gaps 0;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 RVTTHPLHP-KDIVRSIKA[P]RKA 21
 :: ||| | | : ||| | : ||| |
 Db 11 RSTHHPFVRCIFFNERKSPG 30

RESULT 7

Q9TSU6 PRELIMINARY; PRT; 797 AA.

ID Q9TSU6
 AC Q9TSU6;
 DT 01-MAY-2000 (TREMBREL. 13, Created)
 DT 01-MAY-2000 (TREMBREL. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBREL. 19, Last annotation update)

DB BETA MYOSIN HEAVY CHAIN (FRAGMENT).

OS Felis silvestris catus (cat);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI_TaxID=9885;
 RN [1]

RN SEQUENCE FROM N.A.
 RK MEDLINE=2035384; PubMed=10895319;
 RA Meurs K.M., Kittleson M., Spangler E., Ware W.A., Womack J.E.,
 RA Tobin J.A.;
 RT "Nine polymorphisms within the head and hinge region of the feline cardiac beta-myosin heavy chain gene.";
 RT Anim. Genet. 31:231-231(2000).
 DR EMBL; AF08572; ADD51477.1;
 DR EMBL; U9384; ADD51477.1; JOINED.
 DR EMBL; AF001618; ADD51477.1; JOINED.
 DR EMBL; AF001619; ADD51477.1; JOINED.
 DR EMBL; AF002811; ADD51477.1; JOINED.
 DR EMBL; AF002812; ADD51477.1; JOINED.
 DR EMBL; AF002813; ADD51477.1; JOINED.
 DR EMBL; AF00367; ADD51477.1; JOINED.
 DR EMBL; AF00367; ADD51477.1; JOINED.
 DR EMBL; AF00409; ADD51477.1; JOINED.
 DR EMBL; AF00540; ADD51477.1; JOINED.
 DR EMBL; AF00541; ADD51477.1; JOINED.
 DR EMBL; AF005411; ADD51477.1; JOINED.
 DR EMBL; AF005412; ADD51477.1; JOINED.
 DR EMBL; AF00570; ADD51477.1; JOINED.
 DR EMBL; AF008571; ADD51477.1; JOINED.
 DR HSSP; P08795; IMND.
 DR InterPro; IPR00048; IQ.
 DR InterPro; IPR001609; myosin_head.
 DR InterPro; IPR000533; Tropomyosin.
 DR Pfam; PF00052; IQ; 2.
 DR Pfam; PF00053; myosin_head; 1.
 DR PRINTS; PRO0193; MYOSINHEAVY.
 DR PRINTS; PRO0194; TROPOMYOSIN.
 DR PRODOM; PD000355; myosin_head; 1.
 DR SMART; SM00015; IQ; 1.
 DR SMART; SM00424; MSc; 1.
 DR PROSITE; PS50096; IQ; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 797 AA; 91530 MW; 60DD585187328C34 CRC64;

Query Match 36.8%; Score 50; DB 6; Length 797;
 Best Local Similarity 45.0%; Pred. No. 59; Mismatches 7; Indels 0; Gaps 0;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 RVTTHPLHP-KDIVRSIKA[P]RKA 21
 :: ||| | | : ||| | : ||| |
 Db 486 RSTHHPFVRCIFFNERKSPG 505

RESULT 8

Q28699 PRELIMINARY; PRT; 1038 AA.

ID Q28699
 AC Q28699;
 DT 01-NOV-1996 (TREMBREL. 01, Created)
 DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBREL. 19, Last annotation update)

DB BETA CARDIAC MYOSIN HEAVY CHAIN (FRAGMENT).

OS Oryctolagus cuniculus (Rabbit);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Diplopoda; Oryctolagus.
 NCBI_TAXID=9986;
 RN [1]

RN SEQUENCE FROM N.A.
 RK TISSUE-SKELETAL MUSCLE;
 RA Jaenische T., Goldspink G.;
 RT "unpublished.";
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 RN [2] SEQUENCE OF 57-809 FROM N.A.
 RP TISSUE=SKELETAL MUSCLE;

	Query Match	Best Local Similarity	Score	Length	RT
	Matches	9;	Conservative	4;	Pred. No.
				Mismatches	1.5e+02;
QY	2	RVTHPHLPKDVRSIKAPG	21		
Db	663	RSTPHPHVRCLPNETKSPG	682		
RESULT	10				
ID	Q9KR1				
AC	Q9KR1				
DT	01-MAR-2001 (TREMBLrel. 16, Created)				
DT	01-DEC-2001 (TREMBLrel. 16, last sequence update)				
DR	MYOSIN HEAVY CHAIN SLOW ISOFORM.				
DE	MYOC-SLOW.				
GN	SUS scrofa (Pig).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9023;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=LANDRAKE; TISSUE=SKELETAL MUSCLE;				
RA	Chikuni K., Muoya S., Nakajima T.; "Sequencing of the porcine myosin heavy chain slow isoform."				
RT	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.				
RL	EMBL; AB053256; BAB0630.1; -.				
DR	HSSP; P03799; 1MD.				
DR	InterPro; IPR00048; 1Q.				
DR	InterPro; IPR00409; Myosin-N.				
DR	InterPro; IPR00328; Myosin-tail.				
DR	Pfam; PF00063; Myosin_head; 1.				
DR	Pfam; PF02736; Myosin_N; 1.				
DR	Pfam; PF01576; Myosin_tail; 1.				
DR	PRINTS; PR00193; MYOSINHEAVY.				
DR	PRODOM; DD000355; myosin_head; 1.				
DR	SMART; SM00242; MYSC; 1.				
DR	SMART; SM00015; IQ; 1.				
DR	PROSITE; PS50096; IQ; 1.				
SQ	SEQUENCE 1935 AA; 223297 MW; 270556D9A3E86C4A CRC64;				
RESULT	9				
ID	Q9HDS5				
AC	Q9HDS5				
DT	01-MAR-2001 (TREMBLrel. 16, Created)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DR	MYOC-SLOW.				
DR	InterPro; IPR001609; myosin_head.				
DR	InterPro; IPR00048; 1Q.				
DR	InterPro; IPR00328; Myosin-tail.				
DR	Pfam; PF00063; Myosin_head; 1.				
DR	Pfam; PF02736; Myosin_N; 1.				
DR	Pfam; PF01576; Myosin_tail; 1.				
DR	PRINTS; PR00193; MYOSINHEAVY.				
DR	PRODOM; DD000355; myosin_head; 1.				
DR	SMART; SM00242; MYSC; 1.				
DR	SMART; SM00015; IQ; 1.				
DR	PROSITE; PS50096; IQ; 1.				
SQ	SEQUENCE 1935 AA; 223297 MW; 270556D9A3E86C4A CRC64;				
RESULT	11				
ID	Q9BES9				
AC	Q9BES9				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DR	MYOSIN HEAVY CHAIN SLOW.				
GN	MYOC-SLOW.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; OC				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RC	STRAIN=HOLSTEIN; TISSUE=SKELETAL MUSCLE;				

RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.	RA	Strausberg R.;
DR	EMBL; AB059400; BAB40922.1; -.	RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR	HSSP; P08759; IMND.	DR	EMBL; BC003878; AAH33878.1; -.
DR	InterPro; IPR000446; IQ.	DR	HSSP; P01842; 7FAB.
DR	InterPro; IPR001605; myosin_head.	DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR004005; myosin_N.	DR	InterPro; IPR003597; Ig-cl.
DR	InterPro; IPR002938; Myosin_tail.	DR	InterPro; IPR003600; Ig-line.
DR	Pfam; PF00236; Myosin_N; 1.	DR	InterPro; IPR003006; Ig_MHC.
DR	Pfam; PRO1576; Myosin tail; 1.	DR	InterPro; IPR003556; Ig_V.
DR	PRINTS; PR00193; MYOSINHEAVY.	DR	Pfam; PF00047; Ig; 4.
DR	PRODOM; PD000355; myosin_head; 1.	DR	SMART; SM00409; Ig; 2.
DR	SMART; SM00015; IQ; 1.	DR	SMART; SM00406; IgV; 1.
DR	SMART; SM00242; MUSC; 1.	DR	SMART; SM00410; Ig-like; 1.
DR	PROSITE; PS50056; IQ; 1.	DR	PROSITE; PS0290; Ig_MHC; UNKNOWN_1.
SQ	SEQUENCE 1935 AA; 223228 MN; DEA05200BCF42557 CRC64;	SQ	SEQUENCE 468 AA; 51661 MW; 90352328B332ADD CRC64;
RESULT 12		Query Match	Score 36.8%; Score 50; DB 6; Length 1935; Best Local Similarity 45.0%; Pred. No. 1.5e+02; Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
091283		PRELIMINARY;	PT; 1935 AA.
ID	Q91283		
AC	Q91283;		
DT	01-DEC-2001 (TREMBREL. 19, Created)		
DT	01-DEC-2001 (TREMBREL. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)		
DE	BETA MYOSIN HEAVY CHAIN.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	NCBI_TaxId-10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC			
RA	STRAIN-FVB;		
RA	Gulick J.D., Robbins J.;		
RT	"In Vivo Examination of Myosin Heavy Chain Isoform Functionality in the Heart,"		
RT	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY050464; AAL17913.1;		
SQ	SEQUENCE 1935 AA; 222878 MW; 08CDD03573B10CF0 CRC64;		
Query Match	Score 36.8%; Score 50; DB 11; Length 1935; Best Local Similarity 45.0%; Pred. No. 1.5e+02; Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;	Query Match	Score 36.4%; Score 49.5; DB 11; Length 468; Best Local Similarity 46.2%; Pred. No. 40; Matches 12; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
091283		PRELIMINARY;	PT; 473 AA.
ID	Q91283		
AC	Q91283;		
DT	09-DEC-2001 (TREMBREL. 17, Created)		
DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)		
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)		
DE	SIMILAR TO RIKEN CDNA 1810060009 GENE.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	NCBI_TaxId-10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	STRAUBERG R.;		
RA	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; BC003888; AAC03888.1; -.		
DR	HSSP; P01842; 7FAB.		
DR	InterPro; IPR003590; Ig.		
DR	InterPro; IPR003597; Ig-cl.		
DR	InterPro; IPR003600; Ig-like.		
DR	InterPro; IPR003005; Ig-MHC.		
DR	InterPro; IPR003596; Ig-V.		
DR	Pfam; PF00047; Ig; 4.		
DR	SMART; SM00409; Ig; 2.		
DR	SMART; SM00407; IgCl; 3.		
DR	SMART; SM00406; IgV; 1.		
DR	SMART; SM00410; Ig-like; 1.		
DR	PROSITE; PS00200; Ig_MHC; UNKNOWN_1.		
SQ	SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;		
RESULT 13		Query Match	Score 36.4%; Score 49.5; DB 11; Length 473; Best Local Similarity 46.2%; Pred. No. 40; Matches 12; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
091283		PRELIMINARY;	PT; 468 AA.
ID	Q91283		
AC	Q91283;		
DT	01-JUN-2001 (TREMBREL. 17, created)		
DT	01-JUN-2001 (TREMBREL. 17, last sequence update)		
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)		
DE	SIMILAR TO RIKEN CDNA 1810060009 GENE.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	NCBI_TaxId-10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		

DT 01-DEC-2001 (TREMBLrel_19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel_19, Last annotation update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS *Mus musculus* (Mouse).
OC Eukaryota; Metazoa; Chorozata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Mus*.
OX NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC010327; ARI10327.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CRG25F008932AF12 CRC64;

Query Match 36.4%; Score 49.5; DB 11; Length 473;
Best local Similarity 46.2%; Pred. No. 40;
Matches 12; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
Oy 1 CRYTHRHHLKDTRSTAKARG-KRAP 25
| : | : | : | : | : | : |
Db 347 CRVNNKNDLSPPIERTRISKIKGLVRAP 372

Search completed: July 15, 2002, 12:49:27
Job time: 223 sec